# NOVEL GENE ENCODING A DNA REPAIR ENZYME
## AND METHODS OF USE THEREOF
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5    This application is a continuation-in-part
application of US Application 09/463,891 entitled
"Novel Gene Encoding a DNA Repair Endonuclease and
Methods of Use Thereof, filed January 28, 2000, which
is the US National Phase Application of
10   PCT/US98/15828, filed July 28, 1999.  This application
also claims priority under 35 U.S.C. §119(e) from US
Provisional Application 60/053,936 filed July 28,
1997.  The entire disclosures of all of the above-
identified applications are incorporated by reference
15   herein.

**FIELD OF THE INVENTION**

This invention relates to the field of DNA
repair.  Specifically, a novel human gene, its encoded
20   enzyme and methods of use thereof are disclosed.  The
gene may be used beneficially as a marker for genetic
screening, mutational analysis and for assessing drug
resistance in transformed cells.  The encoded enzyme
may be used to advantage in glycosylase assays.

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**BACKGROUND OF THE INVENTION**

Several publications are referenced in this
application in order to more fully describe the state
of the art to which this invention pertains.  The
30   disclosure of each of these publications is
incorporated by reference herein.
Mismatch repair stabilizes the cellular genome by
correcting DNA replication errors and by blocking
recombination events between divergent DNA sequences.
35   The mechanism responsible for strand-specific
correction of mispaired bases has been highly
conserved during evolution.  Eukaryotic homologs of
bacterial MutS and MutL, which are believed to play

key roles in mismatch repair recognition and initiation of repair, have been identified in yeast and mammalian cells. Inactivation of genes encoding these activities results in large increases in

5    spontaneous mutability, and in the case of humans and rodents, predisposition to tumor development.

Lynch syndrome or hereditary nonpolyposis colon cancer (HNPCC) is an autosomal dominant disease, which accounts for approximately 1-5% of all colorectal

10   cancer cases. In this syndrome, colorectal tumors are frequently associated with extracolonic malignancies, such as cancers of the endometrium, stomach, ovary, brain, skin and urinary tract. Tumors from HNPCC patients harbor a genome-wide DNA replication/repair

15   defect. Due to the lack of pathognomonic morphological or biomolecular markers, HNPCC has traditionally posed unique problems to clinicians and geneticists alike, both in terms of diagnosis and clinical management.

20   Recent breakthroughs in molecular biology have partially elucidated the pathogenic mechanism of this syndrome. Germline mutations in any one of five genes encoding proteins that participate in a specialized DNA mismatch repair system give rise to a

25   predisposition for cancer development in HNPCC families. Patients affected by HNPCC carry these mutations in genes which are involved in DNA mismatch repair. The DNA mismatch repair mechanism contributes to mutational avoidance and genetic stability, thus

30   performing a tumor suppressor function. Loss or inactivation of the wild type allele in somatic cells leads to a dramatic increase of the spontaneous mutation rate. This, in turn, results in the accumulation of mutations in other tumor suppressor

35   genes and oncogenes, ultimately leading to neoplastic

transformation.

Microsatellites are repeating sequences that are distributed throughout the human genome, most commonly (A)n/(T)n and (CA)n/(GT)n. Their function is unknown, but they are useful in genetic linkage studies because of their high degree of polymorphism and normally stable inheritance. Several of the genes responsible for HNPCC have been identified using analysis of mutation rate in DNA microsatellites. Mutations of mismatch repair genes can be detected in a subset of sporadic colonic and extracolonic cancers which exhibit variability in the length of microsatellite sequences. This variability is often referred to as microsatellite instability.

Investigators in the field (Peltomaki et al., (1993) *Science* 260:810-812) have discovered that most colorectal cancers from HNPCC patients show microsatellite instability. These studies revealed that the length of microsatellite DNA at different loci varies between tumor DNA and non-tumor DNA from the same patient. The phrase "replication error positive" (RER+) has been used to describe such tumors. It should be noted that only about 70% of HNPCC cases and only about 65% of sporadic tumors with microsatellite instability carry mutations in the known mismatch repair genes (hMSH2, hMLH1, hPMS2, hMSH6 and hPMS1) (Liu et al., (1996) *Nature Medicine* 2:169-174). The remaining 30-35% of the cases have an as yet unidentified mismatch repair genetic defect. Thus, there is a pressing need to identify the other active components in the DNA mismatch repair pathway, as mutations in these genes may result in an increased propensity for cancer.

The Fragile X or Martin Bell syndrome is the most common single recognized form of inherited mental

retardation.  Fifty percent of all X-linked mental
retardation may be attributable to the Fragile X
syndrome.  The disorder is found in all ethnic
groupings with a frequency of 0.3-1 per 1000 males and
0.2-0.6 per 1000 females.  The full clinical syndrome,
which is found in approximately 60% of affected males,
consists of moderate mental retardation with an IQ
typically in the range 35-50, elongated facies with
large everted ears, and macroorchidism.  This syndrome
is unusual in that it is associated with the
appearance of a fragile site on the long arm of the X
chromosome at Xq27.3 (Sutherland, G.R., (1977) *Science*
197:256-266).  This can be visualized cytogenetically
in metaphase chromosomes prepared from lymphocytes of
affected individuals which have been cultured under
conditions of folate deficiency or thymidine stress.
The study of the segregation of polymorphic markers
within fragile X families has confirmed that the
mutation lies in the same region of the X-chromosome
as that exhibiting cytogenetic fragility.

There is an imbalance of penetrance of the
phenotype associated with this syndrome in the
different generations of kindreds in which the
mutation is segregating.  The likelihood of developing
mental impairment depends on an individual's position
in the pedigree.  As the mutation progresses through
the generations, the risk of mental impairment
increases.  These observations are not consistent with
classical X linkage and are collectively known as the
Sherman paradox.  Hypotheses based on these
observations have suggested that the mutation exists
in two forms- a premutation and a full mutation form.
Nonpenetrant individuals are said to carry a
premutation chromosome, that is, a chromosome which
has no abnormal phenotypic effect but which is capable

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of progressing to a fully penetrant mutation on passage through a female oogenesis.

Two alterations in the DNA at the fragile X site have been identified: abnormal amplification of a CpG-rich DNA sequence (a CpG island) and hypermethylation of such sequences. The molecular basis of the amplification is the expansion of a CGG triplet microsatellite into large arrays. In individuals expressing the full clinical phenotype, the DNA in this region becomes hypermethylated, leading to the transcriptional shut down of the gene FMR-1 (fragile X mental retardation 1) which is transcribed across this region. The clinical phenotype is likely caused by a loss of gene expression. It has been postulated that in Fragile X syndrome, expansion of the (CGG)n repeat from premutation to full mutation may be related to an aberrant (misdirected) DNA mismatch repair event. This may be favored by the transient lack of multiple methyl signals in the CGG repeat as well as in flanking single copy sequences during early stages of embryonal development. Similar to Fragile X syndrome, defective DNA mismatch repair may play a role in the expansion of triplet repeats associated with several disorders such as myotonic dystrophy, Huntington's disease, spino-cerebellar ataxias and Kennedy's disease.

The isolation of nucleic acids and proteins which, when mutated, give rise to these various disorders, enables the development of diagnostic and prognostic kits for assessing patients at risk. The biochemical characterization of the genes encoding the components of the DNA mismatch repair system may ultimately facilitate gene replacement therapies for use in the treatment of malignancy and other inherited genetic disorders.

## SUMMARY OF THE INVENTION

This invention provides biological molecules useful for identification, detection, and/or regulation of components in the complex DNA damage recognition/repair pathway. According to one aspect of the invention, an isolated nucleic acid molecule is provided which includes a sequence encoding a methyl CpG binding protein of a size between about 60 and 75 kilodaltons. The encoded protein, referred to herein as MED1 (methyl-CpG binding endonuclease 1; also referred to in the literature as MBD4)) comprises a tripartite structure including an amino terminal methyl-CpG binding domain with significant homology to the rat protein, MeCP2 and the human protein, PCM1, a central region rich in positively-charged amino acids which contains nuclear localization signals, and a carboxy terminal catalytic domain which shares homology with several bacterial endonucleases involved in DNA repair. The protein demonstrates significant binding affinity for hMLH1 and mMSH2. In a preferred embodiment of the invention, an isolated nucleic acid molecule is provided that includes a cDNA encoding a human MED1 protein. In a particularly preferred embodiment, the human MED1 protein has an amino acid sequence the same as Sequence I.D. No. 2. An exemplary nucleic acid molecule of the invention comprises Sequence I.D. No. 1.

According to another aspect of the present invention, an isolated nucleic acid molecule is provided, which has a sequence selected from the group consisting of: (1) Sequence I.D. No. 1; (2) a sequence specifically hybridizing with preselected portions or all of the complementary strand of Sequence I.D. No. 1; a sequence encoding preselected portions of

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Sequence I.D. No. 1, (3) a sequence encoding part or all of a polypeptide having amino acid Sequence I.D. No. 2. Such partial sequences are useful as probes to identify and isolate homologues of the MED1 gene of the invention. Accordingly, isolated nucleic acid sequences encoding natural allelic variants of Sequence I.D. No. 1 are also contemplated to be within the scope of the present invention. The term natural allelic variants will be defined hereinbelow.

In yet another embodiment of the invention, isolated genomic DNA molecules are provided which encode the Med-1 protein of the invention. These nucleic acids (SEQ ID NO: 21 and 22) may be used to advantage in screening assays which identify germline and somatic mutations in the DNA encoding Med-1.

The present invention also provides MED1 genomic nucleic acid of mouse or human origin having a sequence substantially the same as that contained in phage stocks as deposited on 28 July 1998 at the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia 20110-2209 USA, under the terms of the Budapest Treaty with accession numbers: 203073 and 203074.

MED1 polypeptide may conveniently be obtained by introducing expression vectors into host cells in which the vector is functional, culturing the host cells so that the MED1 polypeptide is produced and recovering the MED1 polypeptide from the host cells or the surrounding medium. Vectors comprising nucleic acid according to the present invention and host cells comprising such vectors or nucleic acid form further aspects of the present invention.

According to another aspect of the present invention, an isolated human methyl CpG binding protein is provided which has a deduced molecular

weight of between about 60 kDa and 75 kDa.  The
protein comprises an amino-terminal methyl-CpG binding
domain with significant homology to the rat protein
MeCP2 and the human protein PCM1, a central region

5      rich in positively-charged amino acids which contains
nuclear localization signals, and a carboxy terminal
catalytic domain which shares homology with several
bacterial endonucleases involved in DNA repair.  In a
preferred embodiment of the invention, the protein is

10     of human origin, and has an amino acid sequence the
same as Sequence I.D. No. 2.  In a further embodiment
the protein may be encoded by natural allelic variants
of Sequence I.D. No. 1.  Inasmuch as certain amino
acid variations may be present in a MED1 protein

15     encoded by a natural allelic variant, such proteins
are also within the scope of the invention.

        According to another aspect of the present
invention, antibodies immunologically specific for the
proteins described hereinabove are provided.

20          In yet a further aspect of the invention,
assays are provided for assessing the glycosylase
activity of MED1.  Also provided are methods employing
the MED1 protein to detect transition single-
nucleotide polymorphisms at CpG sites.  Also provided

25     are methods wherein polymerase chain reaction/single
strand conformation polymorphism are utilized to
detect mutations in the MED1 gene.  Methods employing
loss of heterozygosity (LOH) analysis are also
disclosed which may be used to advantage in mutational

30     screening assays for possible MED1 mutations.

        Various terms relating to the biological
molecules of the present invention are used
hereinabove and also throughout the specifications and
claims.  The terms "specifically hybridizing,"

35     "percent similarity" and "percent identity

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(identical)" are defined in detail in the description
set forth below.

With reference to nucleic acids of the
invention, the term "isolated nucleic acid" is
sometimes used.  This term, when applied to DNA,
refers to a DNA molecule that is separated from
sequences with which it is immediately contiguous (in
the 5' and 3' directions) in the naturally occurring
genome of the organism from which it originates.  For
example, the "isolated nucleic acid" may comprise a
DNA or cDNA molecule inserted into a vector, such as a
plasmid or virus vector, or integrated into the DNA of
a prokaryote or eukaryote.

With respect to RNA molecules of the
invention, the term "isolated nucleic acid" primarily
refers to an RNA molecule encoded by an isolated DNA
molecule as defined above.  Alternatively, the term
may refer to an RNA molecule that has been
sufficiently separated from RNA molecules with which
it would be associated in its natural state (i.e., in
cells or tissues), such that it exists in a
"substantially pure" form (the term "substantially
pure" is defined below).

With respect to protein, the term "isolated
protein" or "isolated and purified protein" is
sometimes used herein.  This term refers primarily to
a protein produced by expression of an isolated
nucleic acid molecule of the invention.
Alternatively, this term may refer to a protein which
has been sufficiently separated from other proteins
with which it would naturally be associated, so as to
exist in "substantially pure" form.

The term "substantially pure" refers to a
preparation comprising at least 50-60% by weight the
compound of interest (e.g., nucleic acid,

oligonucleotide, protein, etc.). More preferably, the
preparation comprises at least 75% by weight, and most
preferably 90-99% by weight, the compound of interest.
Purity is measured by methods appropriate for the

5      compound of interest (e.g. chromatographic methods,
agarose or polyacrylamide gel electrophoresis, HPLC
analysis, and the like).

     With respect to antibodies of the invention,
the term "immunologically specific" refers to

10     antibodies that bind to one or more epitopes of a
protein of interest (e.g., MED1), but which do not
substantially recognize and bind other molecules in a
sample containing a mixed population of antigenic
biological molecules.

15          With respect to oligonucleotides, the term
"specifically hybridizing" refers to the association
between two single-stranded nucleotide molecules of
sufficiently complementary sequence to permit such
hybridization under pre-determined conditions

20     generally used in the art (sometimes termed
"substantially complementary"). In particular, the
term refers to hybridization of an oligonucleotide
with a substantially complementary sequence contained
within a single-stranded DNA or RNA molecule of the

25     invention, to the substantial exclusion of
hybridization of the oligonucleotide with single-
stranded nucleic acids of non-complementary sequence.

     The present invention also includes active
portions, fragments, derivatives and functional

30     mimetics of the MED1 polypeptide or protein of the
invention.

     An "active portion" of MED1 polypeptide means a
peptide which is less than said full length MED1
polypeptide, but which retains its essential

35     biological activity, e.g., methyl-CpG DNA binding

and/or endonuclease activity and/or glycosylase
activity.

A "fragment" of the MED1 polypeptide means a
stretch of amino acid residues of at least about five
to seven contiguous amino acids, often at least about
seven to nine contiguous amino acids, typically at
least about nine to thirteen contigous amino acids
and, most preferably, at least about twenty to thirty
or more contiguous amino acids. Fragments of the MED1
polypeptide sequence, antigenic determinants or
epitopes are useful for raising antibodies to a
portion of the MED1 amino acid sequence.

A "derivative" of the MED1 polypeptide or a
fragment thereof means a polypeptide modified by
varying the amino acid sequence of the protein, e.g.
by manipulation of the nucleic acid encoding the
protein or by altering the protein itself. Such
derivatives of the natural amino acid sequence may
involve insertion, addition, deletion or substitution
of one or more amino acids, without fundamentally
altering the essential activity of the wildtype MED1
polypeptide.

"Functional mimetic" means a substance which may
not contain an active portion of the MED1 amino acid
sequence, and probably is not a peptide at all, but
which retains the essential biological activity of
natural MED1 polypeptide.

The nucleic acids, proteins/polypeptides,
peptides and antibodies of the present invention may
be used to advantage as markers for diagnosis and
prognosis of those at risk for colon and other
cancers.  The molecules may also be useful in the
diagnosis and/or treatment of Fragile X syndrome and
other diseases characterized by triplet repeat
expansion.  The MED1 molecules of the invention may

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also be used as research tools in DNA modification/DNA analysis technologies and will facilitate the elucidation of the mechanistic action of the novel genetic and protein interactions involved in the maintenance of DNA fidelity.

Thus, the present invention also provides nucleic acid molecules, polypeptides and/or antibodies as mentioned above for use in medical treatment.

Further, the present invention provides use of a nucleic acid molecule, polypeptide and/or antibody in the preparation of a medicament for treating cancer, in particular, colorectal cancer.

In a further aspect of the present invention, there is provided a kit for detecting mutations in the MED1 gene associated with cancer, or a susceptibility to cancer, the kit comprising one or more nucleic acid probes capable of binding and/or detecting a mutated MED1 nucleic acid. Alternatively, the kit may comprise one or more antibodies capable of specifically binding and/or detecting a mutated MED1 nucleic acid or amino acid sequence or a pair of oligonucleotide primers having sequences corresponding to, or complementary to a portion of the nucleic acid sequence set out in Sequence I. D. No. 1 or 5 for use in amplifying a MED1 nucleic acid sequence or mutant allele thereof.

In yet another aspect of the invention, transgenic animals are provided which are useful for elucidating the role of MED1 in growth and development. Isolation of the mouse genomic DNA also facilitates the production of MED1 knock-out mice.

Aspects and embodiments of the present invention will now be illustrated, by way of example, with reference to the accompanying figures. Further aspects and embodiments will be apparent to those skilled in the art. All documents mentioned in this text are

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incorporated herein by reference.

**BRIEF DESCRIPTION OF THE DRAWINGS**

Figure 1 depicts EGY191 yeast cells cotransformed
with a combination of plasmids as indicated in the
figure along with pSH18-34.  The yeast so transformed
were then selected on uracil-minus, histidine-minus
tryptophan-minus glucose yeast medium to select for
the presence of all plasmids.  Individual
transformants were replated either onto uracil-minus,
histidine-minus, tryptophan-minus, leucine-minus
galactose yeast medium to score activation of the LEU2
reporters (left panel) or onto uracil-minus,
histidine-minus, tryptophan-minus galactose yeast
medium containing 5-bromo-4-chloro-3-indolyl-β-D-
galactopyranoside (X-gal) to score activation of the
LacZ reporters (right panel). Growth on leucine-minus
plates and blue-color formation on X-gal plates
illustrate the specificity of the interaction between
f5/MED1 and hMLH1. All interactions were galactose
specific.  The interaction shown between K-rev-1 and
Krit1 represents a positive control.

Figure 2 depicts a Northern blot showing the
localization of MED1 mRNA in all tested tissues.  A
2.4 kb transcript is observed and high levels of mRNA
expression is detected in heart, skeletal muscle and
pancreas.  The size of the molecular weight standards
is indicated in kb.

Figure 3 shows an alignment of the cDNA of
Sequence I.D. No. 1 and its encoded MED1 protein,
Sequence I.D. No. 2.

Figure 4A depicts homology analysis of the

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deduced amino acid sequence of MED1 and several other endonucleases involved in DNA damage recognition and repair. Figure 4B depicts homology analysis of the deduced amino acid sequence of MED1 and the methyl-CpG binding domain of the rat protein, MeCP2. Figure 4C depicts homology analysis of the deduced amino acid sequence of MED1 and the methyl-CpG binding domain of the human protein, PCM1.

Figure 5 is a schematic diagram illustrating the domain organization of MED1 protein. The methyl-CpG binding domain (MBD) and the endonuclease domain (endo) are highlighted. Numbers indicate amino acid position. The bar below the schematic diagram indicates the portion of the protein encoded by the original f5 clone.

Figure 6 is an autoradiograph showing the results of coupled in vitro transcription and translation of the MED1 open reading frame. Two polypeptides of 70 and 65 kD are synthesized by pcDNA3-MED1 constructs. In control reactions, lacking the MED1 cDNA, these polypeptides are not synthesized.

Figures 7A and 7B show a schematic diagram (Fig. 7A) of carboxy- and amino-terminal hemagglutinin-tagged (HT) MED1 proteins and a Western Blot (Fig. 7B) showing protein expression following transfection of the constructs into NIH 3T3 cells. A band of approximately 72 kD is present in cells transfected with the carboxyterminally tagged MED1-HT. This band co-migrates with the one present in HT-MED1-M1 transfectants, indicating that the first ATG at nucleotide position 142 is the initiation codon in vivo.

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Figure 8 is a partial metaphase spread of human chromosomes showing the chromosomal localization of MED1 by FISH. Hybridization is detected on chromosome 3q21 (arrow). An elongated chromosome 3 is shown in the inset.

Figures 9A and 9B are gels and blots demonstrating the nuclease activity of the recombinant endonuclease domain. Figure 9A is a Coomassie-stained SDS-PAGE showing IPTG induction of the bacterially-expressed 18-22-kD MED1 endonuclease domain (codons 455-580)(arrowhead, left panel). In a parallel SDS-PAGE nuclease activity gel (containing heat-denatured calf thymus DNA), the IPTG-induced 18-22-kD MED1 endonuclease domain is negatively stained with the DNA dye, toluidine blue (arrowhead, right panel). P, pellet of 10,000x $g$ centrifugation; S, supernatant of 10,000x $g$ centrifugation. Figure 9B shows endonuclease activity of recombinant wild-type MED1. The entire wild-type MED1 and a deletion mutant lacking the endonuclease domain (Δendo) were expressed in bacteria, purified by nickel-agarose chromatography and stained with Coomassie following SDS-PAGE (left panel). Increasing amounts of the wild-type and Δendo mutant (22 to 175 ng) were incubated with 500 ng of the 3.9 kb supercoiled plasmid pCR2 (Invitrogen) at 37°C for 30. Reaction products were separated on a 1% agarose gel buffered in 1x TAE and containing 0.25 µg/ml ethidium bromide (right panel). Wild-type MED1, but not Δendo, generated nicked and linearized DNA. M, lambda/HindIII digest size standards; I, input plasmid DNA, incubated with reaction buffer only.

Figure 10A is an autoradiograph showing the results of a mobility shift assay of 293 cell lysates

expressing the fusion protein Flag-MED1/f5.  Flag-
peptide eluates from anti-Flag immunoprecipitations of
Flag-MED1/f5-expressing 293 cells demonstrate binding
activity when incubated with a $^{32}$P-labeled double-
stranded oligonucleotide containing five fully
methylated CpG sites.  A mobility shift assay of
recombinant MED1 MBD (codons 1-154) with methylated
and unmethylated DNA probes is shown in Figure 10B.
The purified MED1 MBD demonstrates binding activity
when incubated with a $^{32}$P-labeled double-stranded
oligonucleotide containing five methylated CpG sites
(lane 2).  Binding is abolished by pre-incubation with
a 100-fold excess of the cold methylated
oligonucleotide (lane 3), but not of the cold
unmethylated oligonucleotide (lane 4).  No binding is
detected when the unmethylated probe is used (lanes
5-8)

Figures 11A and 11B are autoradiographs showing
the coimmunoprecipitation of hMSH2 with Flag-MED1/f5.
Fig. 11A shows a band reacting with the anti-hMSH2
antibody.  Comigration with hMSH2 is detected by
western blotting in anti-FLAG immunoprecipitates from
Flag-MED1/f5 transfected cells but not control cells.
Fig. 11B is a western blot of a parallel gel with the
anti-FLAG antibody confirming expression of the Flag-
MED1/f5 construct in transfected 293 cells.
Co-immunoprecipitation of MED1 and MLH1 from human
cells is shown in Figure 11C.  A band reacting with
the anti-MLH1 antibody and comigrating with MLH1 is
detected by western blotting in anti-hemagglutinin
immunoprecipitates from HT-MED1/CMV5-transfected
HEK-293 cells and not from CMV5-transfected control
cells (upper panel).  Western blotting of a parallel
gel with the anti-hemagglutinin antibody confirms

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expression of the HT-MED1 construct in transfected
HEK-293 cells (lower panel).  Lysis buffers contained
0.5% NP-40 (lanes 1-4), 0.2% NP-40 (lanes 5-6) or 1%
Triton X-100 (lanes 7-8).

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Figure 12 shows a series of MED1 mutations which
have been isolated from colon cancer patients.
Figures 12A and 12B and show MED1 sequencing
electropherograms (ABI) of three colon tumor DNAs and

10    a normal control DNA.  Tumors c220T and c226T harbor
an apparently heterozygous adenine deletion at the
(A)10 track (codons 310-313) with predicted frameshift
and stop at codon 317 (Fig. 12A).  The same mutation
was also found in tumor c18T.  Tumor c215T harbors an

15    apparently heterozygous adenine deletion at the (A)6
track (codons 280-282) with predicted frameshift and
stop at codon 302 (Fig. 12B).  Figure 12C shows a
schematic diagram of the truncated products predicted
to be encoded by the mutant MED1 alleles in the

20    indicated tumors.

Figure 13 is a schematic diagram of the genomic
structure of the human MED1 gene (lambda clone MED1
HGL #16).  The position of the eight exons is

25    indicated.  Numbers above the exon boxes refer to exon
number; numbers below the exon boxes refer to the size
of the exons in base pairs.  Exon 1 and part of the
intervening intron between exon 1 and exon 2 was
cloned by PCR (indicated by the hatched line).  The

30    start (ATG) and stop (TAA) codons are marked.  E:
restriction site for the enzyme EcoRI.

Figure 14 is a blot showing the conservation of
the MED1 gene ("Zooblot").  A low stringency Southern

35    blot of genomic DNA from indicated vertebrate species

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reveals bands cross-hybridizing with a human MED1 cDNA probe in mammals (panel A) and non-mammalian vertebrates (panel B). The migration and size (in kilobase pairs) of the DNA standards are indicated.

Figure 15 shows a schematic of the genomic structure of the mouse MED1 gene (lambda clone MED1 MGL #3). The position of seven exons is indicated. Numbers above the exon boxes refer to exon number; numbers below the exon boxes refer to the size of the exons in base pairs. The size and position of the exon 1 are not well defined (as indicated by the dotted line). The start (ATG) codon is marked. The stop codon is presumably located in exon 8 which is not contained in this lambda clone. E: restriction site for the enzyme EcoRI; S: restriction site for the enzyme SalI.

Figure 16 shows the nucleotide sequence (SEQ ID NO: 5) of the mouse cDNA MED1 sequence assembled by juxtaposition of seven exons derived from the genomic clone MED1 MGL #3. Amino Acid Sequence= SEQ ID NO:29.

Figure 17 shows a comparison of the predicted mouse MED1 protein sequence with the human MED1 protein sequence. Upper sequence: mouse MED1; lower sequence: human MED1. Identical amino acids between the two sequences are indicated by a line, similar amino acids by one (low similarity) or two dots (high similarity).

Figure 18 shows the intron and exon sequences of the mouse genomic clone encoding MED1. Exon sequences are shown in upper case; intron sequences are shown in lower case. The splice donor (gt) and acceptor (ga)

sites are in bold.

Figure 19 shows the intron and exon sequences of the human genomic clone encoding MED1. Exon sequences are shown in upper case; intron sequences are shown in lower case. The splice donor (gt) and acceptor (ga) sites are in bold.

Figures 20 A-D show the results of genetic characterization of MED1, mutational analysis and loss of heterozygosity (LOH) studies. Mutations of *MED1* at coding $(A)_{10}$ (Fig. 20A) and $(A)_6$ (Fig. 20B) tracks in microsatellite instability (MSI) carcinomas and cell lines. Single stranded conformational polymorphism (SSCP) analysis is shown for normal and tumor DNA pairs, MSI (HCT15, HCT116) and microsatellite stable (MSS) (SW620, T84) cell lines, and control normal human placental DNA (h.p.). Arrowheads indicate prominent abnormally migrating bands. HCT116 carries a one-basepair deletion at the $(A)_{10}$ track. Additional cell lines negative for mutations at this track include RKO, LS180, DU145, CaOV-3, SkOV-3, Colo205, Colo320, WiDr, SW403 and SW948. Fig. 20C shows representative autoradiographs of LOH analysis. Case numbers are shown at the top with normal (N) and tumor (T) DNA. Dots mark the positions of alleles. Black and white arrowheads indicate allelic losses and MSI, respectively. PCR products were analyzed on 6% polyacrylamide gels and visualized by auto-radiography. Fig. 20D shows the summary of LOH analysis at 11 LDB microsatellite markers. *Tumor c698T carries a double mutation of the *MED1* $(A)_{10}$ track, as shown by SSCP and DNA sequencing.

Figure 21 depicts a schematic of a MED1 DNA N-glycosylase assay. A double-stranded oligonucleotides bearing a mismatch and $^{32}$P-labeled at the 3' end of the bottom strand is incubated with purified recombinant MED1 protein at 37 °C for 60 min, generating an abasic (AP) site. The reaction is then treated with 100 mM NaOH at 90 °C for 30 min, in order to cleave the sugar-phosphate backbone at the AP site. The resulting reaction product is separated from the longer substrate by electrophoresis on denaturing (sequencing) polyacrylamide gels. The signal is detected by autoradiography.

Figure 22 is an autoradiogram showing that MED1 has a G:T mismatch-specific thymine glycosylase activity. The indicated double-stranded oligonucleotides bearing all possible mismatches and $^{32}$P-labeled on the bottom strand (marked by the asterisk) were treated with purified recombinant MED1 protein at 37 °C for 60 min. The reactions were then treated with 100 mM NaOH at 90 °C for 30 min, in order to cleave the sugar-phosphate backbone at the AP site. A band representing a cleavage product was detected for the G:T-containing oligonucleotide substrate labeled on the thymine-containing strand (lane 4). This result indicates that MED1 has thymine glycosylase activity specific for G:T mismatches. Arrows mark the expected migration of the substrate and product bands.

Figure 23 is an autoradiogram showing that MED1 is a monofunctional glycosylase lacking lyase activity. The indicated fractions from a gel-filtration purification of recombinant MED1 were incubated with the $^{32}$P-labelled, G:T-containing double-

strand oligonucleotide substrate. Following incubation, an aliquot of the reaction was processed with NaOH before electrophoresis (upper panel), whereas the remaining portion was subjected to electrophoresis (lower panel). A product band was detected for fractions 14 through 18 after incubation with alkali; no cleavage product was detected for these fractions when the incubation with alkali was omitted. This indicates that MED1 is a monofunctional glycosylase that lacks a detectable associated lyase activity.

Figure 24 is a schematic diagram depicting the mechanism by which MED1 counteracts mutagenesis by deamination of 5-methylcytosine to thymine, and of cytosine to uracil. Deamination of 5-methylcytosine (M) to thymine (T) at CpG sites generates a G:T mismatch (lower panel), whereas deamination of cytosine (C) to uracil (U) generates a G:U mismatch (upper panel). MED1 thymine and uracil glycosylase activity is the first step in the repair of these mismatches. Failure of MED1-initiated DNA repair leads to G>A (or C>T) mutation after a round of DNA replication.

Figure 25 shows the sequence context of MED1 G:T mismatch-specific thymine glycosylase activity: preference for CpG sites. MED1 was incubated with the indicated G:T containing oligonucleotide substrates, in which the mismatched G followed A, C, G, T or 5-methylcytosine (M). Highest thymine glycosylase activity was detected with CpG/TpG and MpG/TpG substrates, which contained a G:T mismatch in the context of a methylated or unmethylated CpG site. Only low amounts of products were generated with

ApG/TpT, GpG/TpC and TpG/TpA substrates.

Figure 26 is a gel showing that the MED1 catalytic domain is sufficient for glycosylase activity. Increasing amounts of recombinant MED1 catalytic domain (marked "cat. dom.") and of recombinant wild type MED1 protein (marked "entire") were incubated with the $^{32}$P-labelled, G:T-containing double-strand oligonucleotide substrate and the resulting thymine glycosylase activity was evaluated. Arrows mark the expected migration of the substrate and product bands. The isolated catalytic domain and wild type MED1 proteins generated comparable amounts of product. This result indicates that the catalytic domain of MED1 is sufficient for glycosylase activity, whereas the MBD is dispensable.

Figure 27 is an autoradiogram showing that MED1 has a G:U mismatch-specific uracil glycosylase activity. The indicated double-stranded oligonucleotides containing uracil (U) paired with A, C, G, and T, were $^{32}$P-labeled on the bottom strand (marked by the asterisk) and treated with purified recombinant MED1 protein at 37 °C for 60 min. The reactions were then treated with 100 mM NaOH at 90 °C for 30 min, in order to cleave the sugar-phosphate backbone at the AP site. A cleavage product was detected for the G:U-containing oligonucleotide substrate labeled on the uracil-containing strand. This result indicates that MED1 has uracil glycosylase activity specific for G:U mismatches. Arrows mark the expected migration of the substrate and product bands.

Figure 28 is an autoradiogram which shows that MED1 has a 5-fluoruracil glycosylase activity.

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Recombinant MED1 protein was incubated with the
indicated oligonucleotide substrates ^{32}P-labeled on the
bottom strand and containing 5-fluorouracil (F) paired
with A, C, G and T, and the resulting glycosylase
activity was evaluated. MED1 displayed 5-fluorouracil
glycosylase activity specific for G:F mismatches.  The
G:U oligonucleotide substrate constitutes a positive
control.  Arrows mark the expected migration of the
substrate and product bands.

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Figure 29 is an autoradiogram which shows that
MED1 has 3, $N^4$-ethenocytosine glycosylase activity. 3,
$N^4$-ethenocytosine (E) is an exocyclic adduct of
cytosine formed by vinyl chloride and other
carcinogenic compounds, such as ethyl carbamate.  The
structure of E in comparison to cytosine is shown on
the left panel. On the right panel, incubation of
MED1 with an oligonucleotide substrate, containing E
paired with G, unveiled a weak E glycosylase activity.
The G:T oligonucleotide substrate constitutes a
positive control.  Arrows mark the expected migration
of the substrate and product bands.  For this
experiment, the standard MED1 glycosylase assay was
modified in that incubation with NaOH was substituted
by incubation with purified AP-site endonuclease
(APE), which cleaves the sugar-phosphate backbone at
AP sites.  This was necessary since E-containing
oligonucleotides are sensitive to NaOH cleavage even
in the absence of an AP site.

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Figure 30 is a schematic diagram illustrating
detection of transition single nucleotide
polymorphisms at CpG sites (CT-SNPs) with recombinant
MED1 protein.  Two CT-SNP alleles, allele 1 (CpG) and

allele 2 (CpA) can be distinguished by annealing to a CT-SNP probe followed by incubation with MED1, NaOH treatment and electrophoretic separation. Only the heteroduplex containing a G:T mismatch (corresponding

5      to allele 1) will generate a cleavage product, unlike the homoduplex (corresponding to allele 2).


**DETAILED DESCRIPTION OF THE INVENTION**

10      Hereditary Non-Polyposis Colorectal Cancer (HNPCC), or Lynch Syndrome, is an autosomal dominant disorder characterized by early onset colorectal tumors. As noted above, tumors from HNPCC patients harbor a genome-wide DNA replication/repair defect,

15      the hallmark of which is length instability of microsatellite repeat sequences. Patients affected by HNPCC carry a germline mutation in genes involved in DNA mismatch repair, a specialized system which handles base-base mismatches, short

20      insertions/deletions and recombination-derived heteroduplexes (Kolodner, R.D., (1995) *Trends in Biochem. Sci.* 20:397-4053; Modrich and Lahue, (1996) *Annu. Rev. Biochem.* 65:101-133). The mismatch repair pathway contributes to mutational avoidance and

25      genetic stability, thus performing a tumor suppressor function. Loss or inactivation of the wild type allele in somatic cells leads to a dramatic increase of the spontaneous mutation rate. This, in turn, results in the accumulation of mutations in other

30      tumor suppressor genes and oncogenes, ultimately leading to neoplastic transformation (Bellacosa et al., (1996) *Am. J. of Med. Genetics* 62:353-364). Similarly to other genes involved in tumor suppression, mutations of mismatch repair genes can be

35      detected in a subset of sporadic colonic and

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extracolonic cancers which exhibit microsatellite instability (Liu et al., 1996, supra).

Any one of five DNA mismatch repair genes (hMSH2, hMLH1, hPMS2, hMSH6 and hPMS1) is found to be mutated in the germline DNA of HNPCC patients (Liu et al., 1996, supra). These genes encode human homologues of the *E. coli* mismatch repair proteins MutS and MutL, which belong to the methyl-directed mismatch repair system (Kolodner, R.D., 1995, supra). Repair by this system involves 10 biochemical activities and is organized in 3 sequential steps of initiation, excision and resynthesis (Modrich, P., 1991) *Ann. Rev. Genet.* 25:229-253). During initiation, the mismatch is detected and a single-strand cut is made on the newly synthesized DNA strand which contains the mutation. Then, single-strand exonucleases (exo I, exo VII, RecJ) excise a span of about 1-2 kbp containing the mismatch and finally resynthesis by DNA polymerase III takes place. The products of the mutSLH genes mediate the initiation step. MutS detects and binds to the mismatch. Through an interaction with MutL, which likely functions as an interface with MutS, the single-strand endonuclease MutH is activated and cuts the DNA strand carrying the mutation (Modrich, P., 1991, supra).

A similar biochemical pathway has been identified in eukaryotic cells, and it is also characterized by strand-specificity and bidirectional excision capability (Fang and Modrich, (1993) *J. Biol. Chem.* 268:11838-11844). In the bacterial system, MutH has the pivotal role of identifying the newly synthesized strand, i.e. the strand carrying the mutation. Without this function there would be a 50% chance of initiating repair on the parental strand, thereby stabilizing the mutation. MutH identifies and cleaves

the new strand by virtue of its transient lack of
adenine methylation at d(GATC) sites (Modrich, P.,
1991, supra).  Despite its crucial function,
homologues of MutH, i.e., eukaryotic mismatch repair
endonucleases, have not been identified to date.
Furthermore, the molecular determinants of strand
discrimination in eukaryotic cells - which lack
d(GATC) methylation - are not presently known
(Kolodner, R.D., 1995, supra; Modrich and Lahue, 1996,
supra).  In order to gain insight into the mechanisms
of strand recognition, it is essential to identify the
eukaryotic functional homologue of the MutH
endonuclease.  Due to its proposed central role in
mismatch repair, inactivation of this enzyme could be
responsible for at least some cases of HNPCC.

As mentioned previously, aberrant DNA methylation
may also play a role in Fragile X Syndrome.  After
semi-conservative replication of DNA, the mismatch
repair system is able to use the conserved strand as a
template to correct mismatches resulting from
replication errors which are by definition in the
newly synthesized strand.  DNA replication results in
a transient state of hemimethylation in which
methylation occurs only on the template strand.  In
Fragile X Syndrome, the CGG repeats and subsequent
expansion of these repeats may be triggered by
undermethylation leading to misdirection of DNA
mismatch repair.  MED1 encoded proteins may play a
pivotal role in this aberrant DNA replication/repair
event.  As mentioned earlier, this could also be the
case for other diseases associated with repeat
expansion, such as myotonic dystrophy, Huntington's
disease, spino-cerebellar ataxias and Kennedy's
disease.

The genomic and cDNA cloning of MED1, the DNA

molecule of the invention, which encodes a protein
bearing homology to bacterial endonucleases and
glycosylases/lyases is described in detail below.
Analysis of the predicted amino acid sequence of the
MED1 protein suggests a putative mechanism of strand
recognition based on cytosine methylation at CpG
sites. Indeed as confirmed by the data presented
herein, MED1 is a mismatch specific glycosylase. Like
other DNA recognition and repair genes which are
mutated in HNPCC as well as in sporadic cancers with
microsatellite instability, MED1 is a candidate
nucleic acid for cancer genetic testing, both in HNPCC
families and in sporadic cancers with microsatellite
instability. Aberrant MED1 activity may also be
associated with Fragile X Syndrome and other diseases
characterized by triplet repeat expansion.

MED1 possesses thymine and uracil glycosylase
activity that specifically removes thymine and uracil
from G:T and G:U mismatches, respectively. Thus MED1
has functions analogous to those of human thymine
glycosylase TDG and its bacterial homolog, mismatch
uracil glycosylase (MUG). Assays for assessing the
glycosylase activity of MED1 isolated from patients
are disclosed herein. Such assays may be used to
assess for genetic mutations in MED1-encoding nucleic
acids. Altered MED1 glycosylase activity may be
associated with certain forms of cancer. Glycosylase
assays based on MED1 may also be used to assess for
genetic mutations/polymorphisms in nucleic acids as
described further hereinbelow.

Based on its G:T mismatch-specific glycosylase
activity at CpG sites, MED1 appears to counteract
mutagenesis by spontaneous deamination of 5-
methylcytosine to thymine, which indeed would give
rise to a G:T mismatch. Deamination of 5-

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methylcytosine to thymine is a process known to occur spontaneously at measurable rates and constitutes a major mutagenic process. Indeed, CpG sites constitute mutational hot spots in many genes, including the tumor suppressor gene *p53*. Deamination of 5-methylcytosine, if not repaired, would lead to C>T and G>A transitions in the next round of DNA replcication. These transitions at CpG sites are the most frequent mutations in human cancer, including nearly 50% of all germline *p53* mutations in Li-Fraumeni syndrome families and nearly 50% of all somatic *p53* mutations in colorectal cancer. Thus, in another aspect, the invention provides methods for detection of transition single-nucleotide polymorphism at CpG sites (CT-SNPs) between known DNA sequences and those isolated from patients.

Determination of the sequence and chromosomal location of MED1 facilitates LOH analysis of patient DNA to assess for the presence or absence of MED1 encoding nucleic acids. As mentioned previously, loss of MED1 expression may abrogate repair of mismatched DNA which in turn, may ultimately give rise to neoplasia.

## I.   Preparation of MED1-Encoding Nucleic Acid Molecules, MED1 Proteins, and Antibodies Thereto
## A.   Nucleic Acid Molecules

Nucleic acid molecules encoding the MED1 protein of the invention may be prepared by two general methods: (1) Synthesis from appropriate nucleotide triphosphates, or (2) Isolation from biological sources. Both methods utilize protocols well known in the art.

The availability of nucleotide sequence information, such as the full length cDNA having

Sequence I.D. No. 1, enables preparation of an isolated nucleic acid molecule of the invention by oligonucleotide synthesis. Synthetic oligonucleotides may be prepared by the phosphoramidite method employed in the Applied Biosystems 38A DNA Synthesizer or similar devices. The resultant construct may be purified according to methods known in the art, such as high performance liquid chromatography (HPLC). Long, double-stranded polynucleotides, such as a DNA molecule of the present invention, must be synthesized in stages, due to the size limitations inherent in current oligonucleotide synthetic methods. Thus, for example, a 2.4 kb double-stranded molecule may be synthesized as several smaller segments of appropriate complementarity. Complementary segments thus produced may be annealed such that each segment possesses appropriate cohesive termini for attachment of an adjacent segment. Adjacent segments may be ligated by annealing cohesive termini in the presence of DNA ligase to construct an entire 2.4 kb double-stranded molecule. A synthetic DNA molecule so constructed may then be cloned and amplified in an appropriate vector.

Nucleic acid sequences encoding MED1 may be isolated from appropriate biological sources using methods known in the art. In a preferred embodiment, a cDNA clone is isolated from a cDNA expression library of human origin. In an alternative embodiment, utilizing the sequence information provided by the cDNA sequence, genomic clones encoding MED1 may be isolated. Alternatively, cDNA or genomic clones having homology with MED1 may be isolated from other species, such as mouse, using oligonucleotide probes corresponding to predetermined sequences within the MED1 gene.

In accordance with the present invention, nucleic

acids having the appropriate level of sequence homology with the protein coding region of Sequence I.D. No. 1 may be identified by using hybridization and washing conditions of appropriate stringency. For example, hybridizations may be performed, according to the method of Sambrook et al., (supra) using a hybridization solution comprising: 5X SSC, 5X Denhardt's reagent, 0.5-1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and up to 50% formamide. Hybridization is carried out at 37-42ºC for at least six hours. Following hybridization, filters are washed as follows: (1) 5 minutes at room temperature in 2X  SSC and 0.5-1% SDS; (2) 15 minutes at room temperature in 2X  SSC and 0.1% SDS; (3) 30 minutes-1 hour at 37ºC in 1X  SSC and 1% SDS; (4) 2 hours at 42-65º in 1X SSC and 1% SDS, changing the solution every 30 minutes.

One common formula for calculating the stringency conditions required to achieve hybridization between nucleic acid molecules of a specified sequence homology is (Sambrook et al., 1989):

$T_m$ = 81.5°C + 16.6Log [Na+] + 0.41(% G+C) - 0.63 (% formamide) - 600/#bp in duplex

As an illustration of the above formula, using [Na+] = [0.368] and 50% formamide, with GC content of 42% and an average probe size of 200 bases, the $T_m$ is 57°C. The $T_m$ of a DNA duplex decreases by 1 - 1.5°C with every 1% decrease in homology. Thus, targets with greater than about 75% sequence identity would be observed using a hybridization temperature of 42°C. Such a sequence would be considered substantially homologous to the nucleic acid sequence of the present invention.

Nucleic acids of the present invention may be maintained as DNA in any convenient cloning vector.

In a preferred embodiment, clones are maintained in a
plasmid cloning/expression vector, such as pBluescript
(Stratagene, La Jolla, CA), which is propagated in a
suitable E. coli host cell. Genomic clones of the

5  invention encoding the human or mouse MED1 gene may be
maintained in lambda phage FIX II (Stratagene).

MED1-encoding nucleic acid molecules of the
invention include cDNA, genomic DNA, RNA, and
fragments thereof which may be single- or double-

10  stranded. Thus, this invention provides
oligonucleotides (sense or antisense strands of DNA or
RNA) having sequences capable of hybridizing with at
least one sequence of a nucleic acid molecule of the
present invention, such as selected segments of the

15  cDNA having Sequence I.D. No. 1. Such
oligonucleotides are useful as probes for detecting or
isolating MED1 genes.

It will be appreciated by persons skilled in the
art that variants (e.g., allelic variants) of these

20  sequences exist in the human population, and must be
taken into account when designing and/or utilizing
oligos of the invention. Accordingly, it is within
the scope of the present invention to encompass such
variants, with respect to the MED1 sequences disclosed

25  herein or the oligos targeted to specific locations on
the respective genes or RNA transcripts. With respect
to the inclusion of such variants, the term "natural
allelic variants" is used herein to refer to various
specific nucleotide sequences and variants thereof

30  that would occur in a human population. Genetic
polymorphisms giving rise to conservative or neutral
amino acid substitutions in the encoded protein are
examples of such variants. Additionally, the term
"substantially complementary" refers to oligo

35  sequences that may not be perfectly matched to a

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target sequence, but the mismatches do not materially affect the ability of the oligo to hybridize with its target sequence under the conditions described.

Thus, the coding sequence may be that shown in Sequence I.D. No. 1, or it may be a mutant, variant, derivative or allele of this sequence. The sequence may differ from that shown by a change which is one or more of addition, insertion, deletion and substitution of one or more nucleotides of the sequence shown. Changes to a nucleotide sequence may result in an amino acid change at the protein level, or not, as determined by the genetic code.

Thus, nucleic acid according to the present invention may include a sequence different from the sequence shown in Sequence I.D. No. 1 yet encode a polypeptide with the same amino acid sequence.

On the other hand, the encoded polypeptide may comprise an amino acid sequence which differs by one or more amino acid residues from the amino acid sequence shown in Sequence I.D. No. 2. Nucleic acid encoding a polypeptide which is an amino acid sequence mutant, variant, derivative or allele of the sequence shown in Sequence I.D. No. 2 is further provided by the present invention. Nucleic acid encoding such a polypeptide may show greater than 60% homology with the coding sequence shown in Sequence I.D. No. 1, greater than about 70% homology, greater than about 80% homology, greater than about 90% homology or greater than about 95% homology.

Also within the scope of the invention are antisense oligonucleotide sequences based on the MED1 nucleic acid sequences described herein. Antisense oligonucleotides may be designed to hybridize to the complementary sequence of nucleic acid, pre-mRNA or mature mRNA, interfering with the production of

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polypeptides encoded by a given DNA sequence (e.g. either native MED1 polypeptide or a mutant form thereof), so that its expression is reduced or prevented altogether. In addition to the MED1 coding

5    sequence, antisense techniques can be used to target control sequences of the MED1 gene, e.g. in the 5' flanking sequence of the MED1 coding sequence, whereby the antisense oligonucleotides can interfere with MED1 control sequences. The construction of antisense

10   sequences and their use is described in Peyman and Ulman, Chemical Reviews, 90:543-584, (1990), Crooke, Ann. Rev. Pharmacol. Toxical., 32:329-376, (1992), and Zamecnik and Stephenson, Proc. Natl. Acad. Sci., 75:280-284, (1974).

15       The present invention provides a method of obtaining nucleic acid of interest, the method including hybridization of a probe having part or all of the sequence shown in Sequence I.D. No. 1 or a complementary sequence, to target nucleic acid.

20   Hybridization is generally followed by identification of successful hybridization and isolation of nucleic acid which has hybridized to the probe, which may involve one or more steps of PCR.

         Such oligonucleotide probes or primers, as well

25   as the full-length sequence (and mutants, alleles, variants, and derivatives) are useful in screening a test sample containing nucleic acid for the presence of alleles, mutants or variants, especially those that confer susceptibility or predisposition to cancers,

30   the probes hybridizing with a target sequence from a sample obtained from the individual being tested. The conditions of the hybridization can be controlled to minimize non-specific binding, and preferably stringent to moderately stringent hybridization

35   conditions are used. The skilled person is readily

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able to design such probes, label them and devise suitable conditions for hybridization reactions, assisted by textbooks such as Sambrook et al (1989) and Ausubel et al (1992).

5    In some preferred embodiments, oligonucleotides according to the present invention that are fragments of the sequences shown in Sequence I.D. No. 1 or Sequence I.D. No. 5, or any allele associated with cancer susceptibility, are at least about 10

10    nucleotides in length, more preferably at least 15 nucleotides in length, more preferably at least about 20 nucleotides in length. Such fragments themselves individually represent aspects of the present invention. Fragments and other oligonucleotides may be

15    used as primers or probes as discussed but may also be generated (e.g. by PCR) in methods concerned with determining the presence in a test sample of a sequence indicative of cancer susceptibility.

   Methods involving use of nucleic acid in

20    diagnostic and/or prognostic contexts, for instance in determining susceptibility to cancer, and other methods concerned with determining the presence of sequences indicative of cancer susceptibility are discussed below.

25    Nucleic acid according to the present invention may be used in methods of gene therapy, for instance in treatment of individuals with the aim of preventing or curing (wholly or partially) cancer. This too is discussed below.

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**B. Proteins**

   MED1 protein demonstrates methyl-CpG DNA binding and glycosylase activity. A full-length MED1 protein of the present invention may be prepared in a

35    variety of ways, according to known methods. The

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protein may be purified from appropriate sources, e.g., transformed bacterial or animal cultured cells or tissues, by immunoaffinity purification. However, this is not a preferred method due to the low amount of protein likely to be present in a given cell type at any time. The availability of nucleic acid molecules encoding MED1 enables production of the protein using *in vitro* expression methods known in the art. For example, a cDNA or gene may be cloned into an appropriate *in vitro* transcription vector, such as pSP64 or pSP65 for *in vitro* transcription, followed by cell-free translation in a suitable cell-free translation system, such as wheat germ or rabbit reticulocyte lysates. *In vitro* transcription and translation systems are commercially available, e.g., from Promega Biotech, Madison, Wisconsin or BRL, Rockville, Maryland.

Alternatively, according to a preferred embodiment, larger quantities of MED1 may be produced by expression in a suitable prokaryotic or eukaryotic system. For example, part or all of a DNA molecule, such as the cDNA having Sequence I.D. No. 1, may be inserted into a plasmid vector adapted for expression in a bacterial cell, such as *E. coli*. Such vectors comprise the regulatory elements necessary for expression of the DNA in the host cell (e.g. *E. coli*) positioned in such a manner as to permit expression of the DNA in the host cell. Such regulatory elements required for expression include promoter sequences, transcription initiation sequences and, optionally, enhancer sequences.

The MED1 produced by gene expression in a recombinant prokaryotic or eukaryotic system may be purified according to methods known in the art. In a preferred embodiment, a commercially available

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expression/secretion system can be used, whereby the recombinant protein is expressed and thereafter secreted from the host cell, to be easily purified from the surrounding medium. If expression/secretion vectors are not used, an alternative approach involves purifying the recombinant protein by affinity separation, such as by immunological interaction with antibodies that bind specifically to the recombinant protein or nickel columns for isolation of recombinant proteins tagged with 6-8 histidine residues at their N-terminus or C-terminus. Alternative tags may comprise the FLAG epitope or the hemagglutinin epitope. Such methods are commonly used by skilled practitioners.

The MED1 proteins of the invention, prepared by the aforementioned methods, may be analyzed according to standard procedures. For example, such proteins may be subjected to amino acid sequence analysis, according to known methods.

As discussed above, a convenient way of producing a polypeptide according to the present invention is to express nucleic acid encoding it, by use of the nucleic acid in an expression system. The use of expression systems has reached an advanced degree of sophistication today.

Accordingly, the present invention also encompasses a method of making a polypeptide (as disclosed), the method including expression from nucleic acid encoding the polypeptide (generally nucleic acid according to the invention). This may conveniently be achieved by growing a host cell in culture, containing such a vector, under appropriate conditions which cause or allow production of the polypeptide. Polypeptides may also be produced in in vitro systems, such as reticulocyte lysate.

Polypeptides which are amino acid sequence
variants, alleles, derivatives or mutants are also
provided by the present invention. A polypeptide which
is a variant, allele, derivative, or mutant may have

5      an amino acid sequence that differs from that given in
Sequence I.D. No. 2 by one or more of addition,
substitution, deletion and insertion of one or more
amino acids. Preferred such polypeptides have MED1
function, that is to say have one or more of the

10     following properties: methyl-CpG DNA binding activity;
glycosylase activity; binding to MLH1; immunological
cross-reactivity with an antibody reactive with the
polypeptide for which the sequence is given in
Sequence I.D. No. 2; sharing an epitope with the

15     polypeptide for which the sequence is given in
Sequence I.D. No. 2 (as determined for example by
immunological cross-reactivity between the two
polypeptides.

A polypeptide which is an amino acid sequence

20     variant, allele, derivative or mutant of the amino
acid sequence shown in Sequence I.D. No. 2 may
comprise an amino acid sequence which shares greater
than about 35% sequence identity with the sequence
shown, greater than about 40%, greater than about 50%,

25     greater than about 60%, greater than about 70%,
greater than about 80%, greater than about 90% or
greater than about 95%. Particular amino acid sequence
variants may differ from that shown in Sequence I.D.
No.2 by insertion, addition, substitution or deletion

30     of 1 amino acid, 2, 3, 4, 5-10, 10-20, 20-30, 30-40,
40-50, 50-100, 100-150, or more than 150 amino acids.

A polypeptide according to the present
invention may be used in screening for molecules which
affect or modulate its activity or function. Such

35     molecules may be useful in a therapeutic (possibly

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including prophylactic) context.

The present invention also provides antibodies capable of immunospecifically binding to proteins of the invention. Polyclonal antibodies directed toward MED1 may be prepared according to standard methods. In a preferred embodiment, monoclonal antibodies are prepared, which react immunospecifically with various epitopes of MED1. Monoclonal antibodies may be prepared according to general methods of Köhler and Milstein, following standard protocols. Polyclonal or monoclonal antibodies that immunospecifically interact with MED1 can be utilized for identifying and purifying such proteins. For example, antibodies may be utilized for affinity separation of proteins with which they immunospecifically interact. Antibodies may also be used to immunoprecipitate proteins from a sample containing a mixture of proteins and other biological molecules. Other uses of anti-MED1 antibodies are described below.

Antibodies according to the present invention may be modified in a number of ways. Indeed the term "antibody" should be construed as covering any binding substance having a binding domain with the required specificity. Thus, the invention covers antibody fragments, derivatives, functional equivalents and homologues of antibodies, including synthetic molecules and molecules whose shape mimics that of an antibody enabling it to bind an antigen or epitope.

Exemplary antibody fragments, capable of binding an antigen or other binding partner, are Fab fragment consisting of the VL, VH, Cl and CH1 domains; the Fd fragment consisting of the VH and CH1 domains; the Fv fragment consisting of the VL and VH domains of a single arm of an antibody; the dAb fragment which

consists of a VH domain; isolated CDR regions and F(ab')2 fragments, a bivalent fragment including two Fab fragments linked by a disulphide bridge at the hinge region. Single chain Fv fragments are also included.

Humanized antibodies in which CDRs from a non-human source are grafted onto human framework regions, typically with alteration of some of the framework amino acid residues, to provide antibodies which are less immunogenic than the parent non-human antibodies, are also included within the present invention.

## II. Uses of MED1-Encoding Nucleic Acids, MED1 Proteins and Antibodies Thereto

MED1 appears to be an important DNA repair enzyme which may play a role in mismatch repair. Mutations in MED1 are associated with certain forms of colon, pancreatic and endometrial cancer. The MED1 molecules of the invention may be used to advantage in genetic screening assays to identify those patients that may be at risk. Screening assays may also be developed which assess aberrant MED1 activity associated with Fragile X syndrome and other diseases characterized by triplet repeat expansion. Due to its methyl-CpG binding domain, MED1 might be useful in the analysis of genome methylation and of methylation-mediated DNA transcription, replication and repair (for instance, by binding to methylated and non-methylated DNA in a differential manner). Due to its endonuclease and/or glycosylase activity, MED1 is expected to be useful in the context of DNA manipulation technology. The employment of MED1 would be of particular interest in the area of mutation detection. Other endonucleases and glycosylases have been successfully used to detect mutations based on

recognition of cleavage products of heteroduplex
intermediates carrying mismatches (Mashal R.D., Koontz
J. and Sklaar J. Nature Genet. 9: 177-183, 1995; Smith
J. and Modrich P. Proc. Natl. Acad. Sci USA 93:
4374-4379, 1996; Angelis et al., Electrophoresis
20:2133-2138, 1999; Bazar et al., Electrophoresis
20:1141-1148, 1999; Vaughan et al., Genet. Anal.
14:169-175, 1999).

Additionally, MED1 nucleic acids, proteins and
antibodies thereto, according to this invention, may
be used as a research tool to identify other proteins
that are intimately involved in DNA recognition and
repair reactions. Biochemical elucidation of the DNA
recognition and repair capacity of MED1 will
facilitate the development of these novel screening
assays for assessing a patient's propensity for cancer
and genetic disease.

### A. MED1-Encoding Nucleic Acids

MED1-encoding nucleic acids may be used for
a variety of purposes in accordance with the present
invention. MED1-encoding DNA, RNA, or fragments
thereof may be used as probes to detect the presence
of and/or expression of genes encoding MED1 proteins.
Methods in which MED1-encoding nucleic acids may be
utilized as probes for such assays include, but are
not limited to: (1) *in situ* hybridization; (2)
Southern hybridization (3) northern hybridization; and
(4) assorted amplification reactions such as
polymerase chain reactions (PCR).

The MED1-encoding nucleic acids of the
invention may also be utilized as probes to identify
related genes from other animal species. As is well
known in the art, hybridization stringencies may be
adjusted to allow hybridization of nucleic acid probes

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with complementary sequences of varying degrees of homology. Thus, MED1-encoding nucleic acids may be used to advantage to identify and characterize other genes of varying degrees of relation to MED1, thereby enabling further characterization of the DNA repair system. Additionally, they may be used to identify genes encoding proteins that interact with MED1 (e.g., by the "interaction trap" technique), which should further accelerate identification of the components involved in DNA repair.

Nucleic acid molecules, or fragments thereof, encoding MED1 may also be utilized to control the production of MED1, thereby regulating the amount of protein available to participate in DNA repair reactions. Alterations in the physiological amount of MED1 protein may dramatically affect the activity of other protein factors involved in DNA repair.

The availability of MED1 encoding nucleic acids enables the production of strains of laboratory mice carrying part or all of the MED1 gene or mutated sequences thereof. Such mice may provide an in vivo model for cancer. Alternatively, the MED1 sequence information provided herein enables the production of knockout mice in which the endogenous gene encoding MED1 has been specifically inactivated. Methods of introducing transgenes in laboratory mice are known to those of skill in the art. Three common methods include: 1. integration of retroviral vectors encoding the foreign gene of interest into an early embryo; 2. injection of DNA into the pronucleus of a newly fertilized egg; and 3. the incorporation of genetically manipulated embryonic stem cells into an early embryo. Production of the transgenic mice described above will facilitate the molecular elucidation of the role MED1 plays in embryonic

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development and cancer.

A transgenic mouse carrying the human MED1 gene is generated by direct replacement of the mouse MED1 gene with the human gene. These transgenic animals are useful for drug screening studies as animal models for human diseases and for eventual treatment of disorders or diseases associated with biological activities modulated by MED1. A transgenic animal carrying a "knock out" of MED1 is useful for assessing the role of MED1 in maintaining DNA fidelity.

As a means to define the role that MED1 plays in mammalian systems, mice may be generated that cannot make MED1 protein because of a targeted mutational disruption of the MED1 gene.

The term "animal" is used herein to include all vertebrate animals, except humans. It also includes an individual animal in all stages of development, including embryonic and fetal stages. A "transgenic animal" is any animal containing one or more cells bearing genetic information altered or received, directly or indirectly, by deliberate genetic manipulation at the subcellular level, such as by targeted recombination or microinjection or infection with recombinant virus. The term "transgenic animal" is not meant to encompass classical cross-breeding or in vitro fertilization, but rather is meant to encompass animals in which one or more cells are altered by, or receive a recombinant DNA molecule. This molecule may be specifically targeted to a defined genetic locus, be randomly integrated within a chromosome, or it may be extrachromosomally replicating DNA. The term "germ cell line transgenic animal" refers to a transgenic animal in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring

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the ability to transfer the genetic information to offspring. If such offspring, in fact, possess some or all of that alteration or genetic information, then they, too, are transgenic animals.

*The alteration or genetic information may be* foreign to the species of animal to which the recipient belongs, or foreign only to the particular individual recipient, or may be genetic information already possessed by the recipient. In the last case, the altered or introduced gene may be expressed differently than the native gene.

The altered MED1 gene generally should not fully encode the same MED1 protein native to the host animal and its expression product should be altered to a minor or great degree, or absent altogether. However, it is conceivable that a more modestly modified MED1 gene will fall within the compass of the present invention if it is a specific alteration.

The DNA used for altering a target gene may be obtained by a wide variety of techniques that include, but are not limited to, isolation from genomic sources, preparation of cDNAs from isolated mRNA templates, direct synthesis, or a combination thereof.

A type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells may be obtained from pre-implantation embryos cultured in vitro (Evans et al., (1981) Nature 292:154-156; Bradley et al., (1984) Nature 309:255-258; Gossler et al., (1986) Proc. Natl. Acad. Sci. 83:9065-9069). Transgenes can be efficiently introduced into the ES cells by standard techniques such as DNA transfection or by retrovirus-mediated transduction. The resultant transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The introduced ES cells thereafter colonize the embryo and contribute

to the germ line of the resulting chimeric animal.

One approach to the problem of determining the contributions of individual genes and their expression products is to use isolated MED1 genes to selectively inactivate the wild-type gene in totipotent ES cells (such as those described above) and then generate transgenic mice. The use of gene-targeted ES cells in the generation of gene-targeted transgenic mice was described, and is reviewed elsewhere (Frohman et al., (1989) Cell 56:145-147; Bradley et al., (1992) Bio/Technology 10:534-539).

Techniques are available to inactivate or alter any genetic region to a mutation desired by using targeted homologous recombination to insert specific changes into chromosomal alleles. However, in comparison with homologous extrachromosomal recombination, which occurs at a frequency approaching 100%, homologous plasmid-chromosome recombination was originally reported to only be detected at frequencies between $10^{-6}$ and $10^{-3}$. Nonhomologous plasmid-chromosome interactions are more frequent, occurring at levels $10^5$-fold to $10^2$-fold greater than comparable homologous insertion.

To overcome this low proportion of targeted recombination in murine ES cells, various strategies have been developed to detect or select rare homologous recombinants. One approach for detecting homologous alteration events uses the polymerase chain reaction (PCR) to screen pools of transformant cells for homologous insertion, followed by screening of individual clones. Alternatively, a positive genetic selection approach has been developed in which a marker gene is constructed which will only be active if homologous insertion occurs, allowing these recombinants to be selected directly. One of the most

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powerful approaches developed for selecting homologous
recombinants is the positive-negative selection (PNS)
method developed for genes for which no direct
selection of the alteration exists.  The PNS method is
more efficient for targeting genes which are not
expressed at high levels because the marker gene has
its own promoter.  Non-homologous recombinants are
selected against by using the Herpes Simplex virus
thymidine kinase (HSV-TK) gene and selecting against
its nonhomologous insertion with effective herpes
drugs such as gancyclovir (GANC) or (1-(2-deoxy-2-
fluoro-B-D arabinofluranosyl)-5-iodouracil, (FIAU).
By this counter selection, the number of homologous
recombinants in the surviving transformants can be
increased.

As used herein, a "targeted gene" or "knock-out"
is a DNA sequence introduced into the germline or a
non-human animal by way of human intervention,
including but not limited to, the methods described
herein.  The targeted genes of the invention include
DNA sequences which are designed to specifically alter
cognate endogenous alleles.

Methods of use for the transgenic mice of the
invention are also provided herein.  Therapeutic
agents for the treatment or prevention of cancer may
be screened in studies using MED1 transgenic mice.

In another embodiment of the invention, MED1
knockout mice may be used to produce an array of
monoclonal antibodies specific for MED1 protein.

As described above, MED1-encoding nucleic acids
are also used to advantage to produce large quantities
of substantially pure MED1 protein, or selected
portions thereof.

## B.  MED1 Protein and Antibodies

Purified MED1, or fragments thereof, may be used to produce polyclonal or monoclonal antibodies which also may serve as sensitive detection reagents for the presence and accumulation of MED1 (or complexes containing MED1) in mammalian cells. Recombinant techniques enable expression of fusion proteins containing part or all of the MED1 protein. The full length protein or fragments of the protein may be used to advantage to generate an array of monoclonal antibodies specific for various epitopes of the protein, thereby providing even greater sensitivity for detection of the protein in cells.

Polyclonal or monoclonal antibodies immunologically specific for MED1 may be used in a variety of assays designed to detect and quantitate the protein. Such assays include, but are not limited to: (1) flow cytometric analysis; (2) immunochemical localization of MED1 in tumor cells; and (3) immunoblot analysis (e.g., dot blot, Western blot) of extracts from various cells. Additionally, as described above, anti-MED1 antibodies can be used for purification of MED1 (e.g., affinity column purification, immunoprecipitation).

From the foregoing discussion, it can be seen that MED1-encoding nucleic acids, MED1 expressing vectors, MED1 proteins and anti-MED1 antibodies of the invention can be used to detect MED1 gene expression and alter MED1 protein accumulation for purposes of assessing the genetic and protein interactions involved in the recognition and repair of DNA damage.

Exemplary approaches for detecting MED1 nucleic acid or polypeptides/proteins include:

a) comparing the sequence of nucleic acid in the sample with the MED1 nucleic acid sequence to

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determine whether the sample from the patient contains mutations; or

b) determining the presence, in a sample from a patient, of the polypeptide encoded by the MED1 gene and, if present, determining whether the polypeptide is full length, and/or is mutated, and/or is expressed at the normal level; or

c) using DNA restriction mapping to compare the restriction pattern produced when a restriction enzyme cuts a sample of nucleic acid from the patient with the restriction pattern obtained from normal MED1 gene or from known mutations thereof; or,

d) using a specific binding member capable of binding to a MED1 nucleic acid sequence (either normal sequence or known mutated sequence), the specific binding member comprising nucleic acid hybridizable with the MED1 sequence, or substances comprising an antibody domain with specificity for a native or mutated MED1 nucleic acid sequence or the polypeptide encoded by it, the specific binding member being labelled so that binding of the specific binding member to its binding partner is detectable; or,

e) using PCR involving one or more primers based on normal or mutated MED1 gene sequence to screen for normal or mutant MED1 gene in a sample from a patient.

A "specific binding pair" comprises a specific binding member (sbm) and a binding partner (bp) which have a particular specificity for each other and which in normal conditions bind to each other in preference to other molecules. Examples of specific binding pairs are antigens and antibodies, ligands and receptors and complementary nucleotide sequences. The skilled person is aware of many other examples and they do not need to be listed here. Further, the term "specific binding pair" is also applicable where either or both of the

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specific binding member and the binding partner .
comprise a part of a large molecule. In embodiments in
which the specific binding pair comprises nucleic acid
sequences, they will be of a length to hybridize to

5  each other under conditions of the assay, preferably
greater than 10 nucleotides long, more preferably
greater than 15 or 20 nucleotides long.

In most embodiments for screening for cancer
susceptibility alleles, the MED1 nucleic acid in the

10  sample will initially be amplified, e.g. using PCR, to
increase the amount of the analyte as compared to
other sequences present in the sample.  This allows
the target sequences to be detected with a high degree
of sensitivity if they are present in the sample. This

15  initial step may be avoided by using highly sensitive
array techniques that are becoming increasingly
important in the art.

The identification of the MED1 gene and its
association with cancer paves the way for aspects of

20  the present invention to provide the use of materials
and methods, such as are disclosed and discussed
above, for establishing the presence or absence in a
test sample of a variant form of the gene, in
particular an allele or variant specifically

25  associated with cancer, especially colorectal,
pancreatic, or endometrial cancer. This may be for
diagnosing a predisposition of an individual to
cancer. It may be for diagnosing cancer of a patient
with the disease as being associated with the gene.

30  This allows for planning of appropriate
therapeutic and/or prophylactic measures, permitting
stream-lining of treatment.  The approach further
stream-lines treatment by targeting those patients
most likely to benefit.

35  According to another aspect of the invention,

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methods of screening drugs for cancer therapy to identify suitable drugs for restoring MED1 product functions are provided. A major problem in cancer treatment is the development of drug resistance or ionizing radiation resistance by the tumor cells which eventually leads to failure of therapy. Recent studies have revealed that inactivation of DNA mismatch repair is an important mechanism of resistance to many chemotherapeutic drugs used in the clinic (Fink D., Aebi S. and Howell S.B. (1998). Clinical Cancer Res. 4: 1-6). In fact, a functional mismatch repair system appears to be required for killing by many alkylating agents and platinum compounds. Resistance/tolerance to those agents is associated with loss of expression or function of mismatch repair genes: in the absence of a functional mismatch repair system, DNA damage accumulates but fails to trigger apoptosis (Fink D., Aebi S. and Howell S.B. (1998), *supra*). Defects in DNA mismatch repair genes (hMLH1, hPMS2, hMSH2 and hMSH6) have been found in cell lines and primary tumors resistant to those chemotherapeutic agents. Thus, loss of MED1 function/expression may be associated with changes in tumor drug sensitivity. Restoration of MED1 function by gene transfer or by pharmacological means would be expected to modulate resistance to treatment.

The MED1 polypeptide or fragment employed in drug screening assays may either be free in solution, affixed to a solid support or within a cell. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant polynucleotides expressing the polypeptide or fragment, preferably in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One

may determine, for example, formation of complexes between a MED1 polypeptide or fragment and the agent being tested, or examine the degree to which the formation of a complex between a MED1 polypeptide or fragment and a known ligand is interfered with by the agent being tested.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the MED1 polypeptides and is described in detail in Geysen, PCT published application WO 84/03564, published on Sep. 13, 1984. Briefly stated, large numbers of different, small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with MED1 polypeptide and washed. Bound MED1 polypeptide is then detected by methods well known in the art.

Purified MED1 can be coated directly onto plates for use in the aforementioned drug screening techniques. However, non-neutralizing antibodies to the polypeptide can be used as capture antibodies to immobilize the MED1 polypeptide on the solid phase.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of specifically binding the MED1 polypeptide compete with a test compound for binding to the MED1 polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants of the MED1 polypeptide.

A further technique for drug screening involves the use of host eukaryotic cell lines or cells (such as described above) which have a nonfunctional MED1 gene. These host cell lines or cells are defective at

the MED1 polypeptide level. The host cell lines or
cells are grown in the presence of drug compound. The
rate of growth of the host cells is measured to
determine if the compound is capable of regulating the

5      growth of MED1 defective cells.

The goal of rational drug design is to produce
structural analogs of biologically active polypeptides
of interest or of small molecules with which they
interact (e.g., agonists, antagonists, inhibitors) in

10     order to fashion drugs which are, for example, more
active or stable forms of the polypeptide, or which,
e.g., enhance or interfere with the function of a
polypeptide in vivo. See, e.g., Hodgson, (1991)
Bio/Technology 9:19-21. In one approach, one first

15     determines the three-dimensional structure of a
protein of interest (e.g., MED1 polypeptide) or, for
example, of the MED1-DNA complex, by x-ray
crystallography, by nuclear magnetic resonance, by
computer modeling or most typically, by a combination

20     of approaches. Less often, useful information
regarding the structure of a polypeptide may be gained
by modeling based on the structure of homologous
proteins. An example of rational drug design is the
development of HIV protease inhibitors (Erickson et

25     al., (1990) Science 249:527-533). In addition,
peptides (e.g., MED1 polypeptide) may be analyzed by
an alanine scan (Wells, (1991) Meth. Enzym. 202:390-
411). In this technique, an amino acid residue is
replaced by Ala, and its effect on the peptide's

30     activity is determined. Each of the amino acid
residues of the peptide is analyzed in this manner to
determine the important regions of the peptide.

It is also possible to isolate a target-specific
antibody, selected by a functional assay, and then to

35     solve its crystal structure. In principle, this

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approach yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original molecule. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced banks of peptides. Selected peptides would then act as the pharmacore.

Thus, one may design drugs which have, e.g., improved MED1 polypeptide activity or stability or which act as inhibitors, agonists, antagonists, etc. of MED1 polypeptide activity. By virtue of the availability of cloned MED1 sequences, sufficient amounts of the MED1 polypeptide may be made available to perform such analytical studies as x-ray crystallography. In addition, the knowledge of the MED1 protein sequence provided herein will guide those employing computer modeling techniques in place of, or in addition to x-ray crystallography and nuclear magnetic resonance (NMR) spectroscopy.


**III Therapeutics**

**A. Pharmaceuticals and Peptide Therapies**

The MED1 polypeptides/proteins, antibodies, peptides and nucleic acids of the invention can be formulated in pharmaceutical compositions. These compositions may comprise, in addition to one of the above substances, a pharmaceutcally acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the active ingredient. The

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precise nature of the carrier or other material may
depend on the route of administration, e.g. oral,
intravenous, cutaneous or subcutaneous, nasal,
intramuscular, intraperitoneal routes.

5        Whether it is a polypeptide, antibody, peptide,
nucleic acid molecule, small molecule or other
pharmaceutically useful compound according to the
present invention that is to be given to an
individual, administration is preferably in a
10       "prophylactically effective amount" or a
"therapeutically effective amount" (as the case may
be, although prophylaxis may be considered therapy),
this being sufficient to show benefit to the
individual.

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### B.    Methods of Gene Therapy

As a further alternative, the nucleic acid
encoding the authentic biologically active MED1
polypeptide could be used in a method of gene therapy,
20       to treat a patient who is unable to synthesize the
active "normal" polypeptide or unable to synthesize it
at the normal level, thereby providing the effect
elicited by wild-type MED1 and suppressing the
occurrence of "abnormal" MED1 lacking the ability to
25       perform or effect DNA repair.

Vectors such as viral vectors have been used in
the prior art to introduce genes into a wide variety
of different target cells. Typically the vectors are
exposed to the target cells so that transformation can
30       take place in a sufficient proportion of the cells to
provide a useful therapeutic or prophylactic effect
from the expression of the desired polypeptide. The
transfected nucleic acid may be permanently
incorporated into the genome of each of the targeted
35       tumor cells, providing long lasting effect, or

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alternatively the treatment may have to be repeated periodically.

A variety of vectors, both viral vectors and plasmid vectors are known in the art, see US Patent No. 5,252,479 and WO 93/07282. In particular, a number of viruses have been used as gene transfer vectors, including papovaviruses, such as SV40, vaccinia virus, herpes viruses including HSV and EBV, and retroviruses. Many gene therapy protocols in the prior art have employed disabled murine retroviruses.

Gene transfer techniques which selectively target the MED1 nucleic acid to colorectal tissues are preferred. Examples of this include receptor-mediated gene transfer, in which the nucleic acid is linked to a protein ligand via polylysine, with the ligand being specific for a receptor present on the surface of the target cells.

The following examples are provided to illustrate certain embodiments of the invention. They are not intended to limit the invention in any way.


**EXAMPLE I**

The methods described below have been used to advantage to isolate the MED1 encoding nucleic acids of the invention.

**A.   Interaction trap screen, cDNA and genomic DNA isolation.**

Yeast interaction trap screening (Gyuris et al., (1993) *Cell* 75:791-803; Golemis et al., (1996) Yeast Interaction Trap/Two Hybrid Systems to Identify Interacting Proteins, Unit 20.1.1-20.1.28 in *Current Protocols in Molecular Biology*, eds. Ausubel, F.M. et al., John Wiley & Sons, NY) was used to isolate cDNAs encoding proteins able to interact with hMLH1. The hMLH1 open reading frame was inserted into the

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polylinker of the pEG202 vector (Golemis et al., 1996, supra). The resulting "bait" construct pEG202-t-hMLH1 expresses the hMLH1 protein (amino acids 1-756) as a carboxyterminal fusion to the LexA DNA binding protein. *Saccharomyces cerevisiae* strain EGY191 (Estojak et al., (1995) *Mol. Cell Bio.* 15:5820-5829) was transformed with the bait construct and with the LacZ reporter plasmid pSH18-34 (Golemis et al., 1996, supra).

The EGY191/pSH18-34/pEG202-t-hMLH1 cells were supertransformed with a human fetal brain cDNA library constructed in the vector pJG4-5. This vector directs the synthesis of proteins fused to the B42 transcriptional activator domain (Ruden et al., (1991) *Nature* 350:25-252) and the expression is controlled by the galactose-inducible GAL1 promoter. Approximately $4 \times 10^5$ independent transformants were obtained in yeast and used for screening. For selection of the positive interactors, the supertransformed cells were cultured on leucine-minus / galactose solid medium. Colonies growing on this medium after 3-5 days incubation were subcultured on leucine-minus or X-Gal media containing either glucose or galactose as a carbon source. Twenty-two colonies growing on leucine-minus / galactose but not leucine-minus / glucose medium and turning blue on X-Gal / galactose but not X-Gal / glucose plates were further characterized.

Plasmid DNA encoding putative hMLH1 interactors was isolated from these colonies (clones f1 through f22), transferred first to KC8 and then to XL-1 blue *E. coli* strains, and sequenced. These and subsequent sequencing reactions were performed on double stranded DNA with the ABI automated sequencer 377 using dye terminator chemistry (Perkin Elmer). Sequence

assembling and analysis was performed with the
Genetics Computer Group software (Genetics Computer
Group, 1994). Since the f5 clone (later named MED1)
was shorter (0.8 kb 3' of B42) than the mRNA
transcript detected in human tissues by Northern blot
analysis (approximately 2.4 kb), a f5-derived probe
was used to screen three additional cDNA lambda
libraries. The libraries, derived from human fetal
brain (Stratagene and Clontech) and from the ovarian
cancer cell line C200 (gift of Drs. A. Godwin and G.
Kruh), were screened following standard procedures as
previously described (Bellacosa et al., 1994, supra).

Screening of a human genomic DNA library prepared
in the lambda phage FIX II (Stratagene) with the
f5/MED1 cDNA probe yielded six clones. One of these
clones (# 16) was further characterized and subcloned
in plasmid vectors. Sequence analysis of the
subclones and comparison to the MED1 cDNA sequence
allowed mapping of seven MED1 exons (exons 2 through
8, Fig. 13). The remaining exon (exon 1) and the
intervening intron between exon 1 and exon 2 was
cloned by PCR utilizing human genomic DNA as template
and the primers of Sequence I.D. No. 6 and 20. SEQ ID
NO: 20 is CAAATCTTCCTGCTGTCTTCC which maps within exon
2. Table I provides suitable primer sets for
amplifying exons of the MED1 gene.

This human genomic clone has been deposited with
the American Type Culture Collection, 10801 University
Blvd., Manassas, VA 20110-2209 on July 28, 1998 under
the terms of the Budapest Treaty, Accession Number:
203074. The sequence of the human genomic clone is
shown in Figure 19, SEQ ID NO:22.

## TABLE I.    OLIGONUCLEOTIDE PRIMERS FOR MED1

| | 5' primer | 3' primer |
|---|---|---|
| exon 1 | GTCTGGGGCGCTTTCGCAA (SEQ ID NO:6) | CCACACACTGTCCACTCTCCCG (SEQ ID NO:7) |
| exon 2 | ACTCCCATAGCACAAGACTGG (SEQ ID NO:8) | GCTATGCTCCCACTACCTGC (SEQ ID NO:9) |
| exon 3 | CCCTTCTATTTACTAGCAGTA (SEQ ID NO:10) | GATGCAGCATATAAATTTCTC (SEQ ID NO:11) |
| exons 4 and 5 | TGCATCCCTCAATATTGCTTT (SEQ ID NO:12) | TCAATTCAGTGCTTTCTCCCT (SEQ ID NO:13) |
| exon 6 | AGCCCACCTGGAGTCTTGTAA (SEQ ID NO:14) | AAAGTTTAAGGTGTGGCTCTC (SEQ ID NO:15) |
| exon 7 | GAAGCTGACCTGATAATGTGG (SEQ ID NO:16) | CTTATTTTGCCTCAGAGACCA (SEQ ID NO:17) |
| exon 8 | TATCGTAATGTACTGTCCCCC (SEQ ID NO:18) | GCTTTAGCAAGGCTGATAGAA (SEQ ID NO:19) |

Screening at low stringency of a mouse 129/SVJ strain genomic DNA library prepared in the lambda phage FIX II (Stratagene) with the same HindIII-HindIII fragment derived from the human MED1 cDNA probe (from nucleotide 1513-1935 of SEQ ID NO: 1) yielded one clone. This clone (#3) was further characterized and subcloned in plasmid vectors. Sequence analysis of the subclones and comparison to the human MED1 cDNA and genomic sequence allowed mapping of seven mouse MED1 exons (exons 1 through 7. Fig. 15). Assembling of the mouse MED1 exons allowed the derivation of a partial sequence of the mouse MED1 cDNA (Figs. 16A and 16B). From the latter sequence a partial predicted amino acid sequence of the mouse MED1 protein was derived and it was shown to be highly conserved by comparison to the human MED1 protein sequence (Fig. 17). This mouse genomic clone has been deposited with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209 on July 28, 1998 under the terms of the Budapest Treaty, Accession Number:203073. The sequence of the mouse genomic clone is shown in Figure 18, SEQ ID NO:21.

### B.    Northern and Southern blot analysis.

A multiple tissue northern blot of poly-A

selected RNA (Clontech) was hybridized under high-stringency conditions to a $^{32}$P-labeled 0.8 kb f5 probe. The blot was washed to a final stringency of 0.1 x SSC/0.1% SDS (1 x SSC is 0.15 M NaCl/0.015 M sodium citrate) at 65°C for 40 minutes, and then exposed to X-ray film (Kodak X-Omat AR) at -70°C.

For the "Zoo" blot experiment, genomic DNA prepared from vertebrate species was digested with the restriction enzyme HindIII (New England Biolabs), separated on a 0.8% agarose gel and transferred to a nylon membrane. The membrane was hybridized to a $^{32}$P-labelled human MED1 cDNA probe (HindIII-HindIII fragment from nucleotide 1513 to nucleotide 1935 of the Sequence I.D. No. 1). Hybridization was performed in a solution containing 35% formamide, 6x SSC, 5x Denhardt's solution, 20 mM sodium phosphate pH 6.5, 20 micrograms/ml of sheared E. coli genomic DNA and 0.5% sodium dodecyl sulfate (SDS). The filter was washed twice at room temperature and twice at 65°C in a solution containing 4x SSC and 0.1% SDS. Hybridization signals were revealed by autoradiography.

Hybridization of the HindIII-HindIII fragment probe (from nucleotide 1513 to nucleotide 1935 of the Sequence I.D. No. 1) at low stringency to a "zoo" blot revealed conservation of the MED1 gene among vertebrates. See Figure 14.


**C.   In vitro transcription and translation.**

Coupled in vitro transcription and translation was conducted with a rabbit reticulocyte lysate- and T7 RNA polymerase-based kit (Promega), following the manufacturer's recommendations and employing $^{35}$S-methionine (Amersham).

## D. Cell culture, expression constructs, and transfections.

NIH 3T3 cells were cultured in Dulbecco's modified Eagle's medium supplemented with 10% calf serum, penicillin (50 units/ml), streptomycin (50µg/ml), and kanamycin (100 µg/ml). The expression constructs of MED1 were generated in the CMV promoter-based CMV5 vector, a derivative of CMV4 (Andersson et al., (1989) *J. Biol. Chem.* 264:8222-8229). For construction of the hemagglutinin epitope carboxy-terminally tagged MED1 plasmid, the MED1 cDNA was inserted in place of the Gfi-1 ZN mutant construct open reading frame (Grimes et al. (1996) *Mol. Cell Bio.* 16:6263-6272), a gift of Dr. Leighton Grimes. For construction of the hemagglutinin epitope amino terminally-tagged MED1 plasmids M1 and M2, a XbaI site was inserted by polymerase chain reaction immediately upstream of the ATG codons at nucleotide positions 142 and 262, respectively. Then the MED1 open reading frame, excised with XbaI and NsiI (blunted), was inserted in place of the Akt gene in the CMV5 hemagglutinin tag·Akt construct (Datta et al., (1996) *J. Biol. Chem.* 271:30835-30839).

Transient transfections of NIH 3T3 cells seeded in 6-well plates at 0.15 x $10^6$ cells/well were carried out using 1.5 µg of DNA and 6 µl of lipofectamine (Life Technologies, Inc.), following the manufacturer's protocol. Forty-eight hours after transfection, cells were washed twice with Dulbecco's phosphate buffered saline and then lysed with RIPA buffer (10mM sodium phosphate pH 7.0, 150mM NaCl, 1% w/v sodium deoxycholate, 1% v/v Nonidet P-40, 0.1% w/v sodium dodecylsulfate, 1mM phenylmethylsulfonyl-fluoride, 2µg/ml aprotinin, 2µg/ml leupeptin, 50mM NaF, 1mM sodium pyrophosphate, 1mM sodium

orthovanadate, 1mM dithiothreitol, and 2mM EDTA).

### E.  Western blotting.

Cell lysates were separated by sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE) in 8.5% gels and transferred to Immobilon P membranes (Millipore) by electroblotting with a Genie apparatus (Idea Scientific Co.) in a buffer containing 25mM Tris-HCl pH 8, 190mM glycine and 20% v/v methanol. Following overnight incubation in 5% dry milk in Tris-buffered saline (TBS: 0.9% w/v NaCl, 10mM Tris-HCl pH 7.4, 0.05% w/v MgCl$_2$), the membrane was incubated for 1 hour at room temperature with the anti-hemagglutinin tag monoclonal antibody 12CA5 (Boehringer) in 2% dry milk in TBS. After three 10-minute washes in TBS supplemented with 0.1% v/v Tween-20, the membrane was incubated for 40 minutes at room temperature with an anti-mouse secondary antibody conjugated to horseradish peroxidase (Amersham). Following washing, the bound secondary antibody was detected by enhanced chemiluminescence (Amersham).

### F.  Fluorescence in situ hybridization.

Metaphase spreads from normal human lymphocytes were prepared according to published methods (Fan et al. (1990) *Proc. Natl. Acad. Sci.* 87:6223-6227). Nick translation was used to label a MED1 genomic DNA subclone with biotin-16-dUTP. Three hundred ng of the probe were then mixed with 150 µg of human Cot-1 DNA (Life Technologies Inc.) and 50 µg salmon sperm DNA to block repetitive elements. The DNA was denatured at 75°C for 5 minutes and then reannealed for 1 hour at 37°C prior to hybridization to metaphase spreads overnight at 37°C. The MED1 signal was detected with fluorescein isothiocyanate-labeled avidin (Oncor),

whereas the chromosomes were counterstained with propidium iodide (Oncor). Metaphase spreads were observed using a Zeiss Axiophot microscope and images were captured by a cooled CCD camera (Photometrics) connected to a computer workstation. To identify the precise chromosomal location of the probe, the separate digitized images of FITC and propidium iodide were merged using Oncor version 1.6 software.

**G.  Electromobility shift analysis**

Transient transfections of 293 cells seeded in 10-cm dishes were carried out using 12 µg of DNA and 48 µl lipofectamine (Life Technologies, Inc.), following the manufacturer's protocol. Seventy-two hours after transfections, cells were washed twice with Dulbecco's phosphate buffered saline and then lysed with NP-40 lysis buffer (0.5% Nonidet P-40, 10% glycerol, 137 mM NaCl, 20 mM Tris-HCl, pH 7.4) containing 1 mM phenylmethylsulfonylfluoride, 2 µg/ml aprotinin, 2 µg/ml leupeptin, 1 mM NaF, 1 mM sodium pyrophosphate, 1 mM sodium orthovanadate, and 1 mM dithiothreitol. Nuclei were disrupted by sonication with a sonic dismembrator (Fisher). Flag-MED1 was immunoprecipitated from the cell lysates with an anti-Flag antibody coupled to agarose beads (Kodak) and then eluted in a 50 µl volume with a solution containing a molar excess of Flag-peptide (Kodak) in electromobility shift analysis (EMSA) buffer (10 mM Tris-HCl, pH 7.5, 50 mM NaCl, 0.5 mM EDTA, 5% glycerol). A double stranded oligonucleotide containing five fully methylated CpG sites was generated by annealing the following oligonucleotides (M= 5-methylcytosine):

Sequence I. D. No. 3:

5'-GCGAATTCMGTGCGAMGAAGCMGGACGATMGACCAGMGCTCGAGCA-3'

Sequence I. D. No. 4:

5'-GTGCTCGAGMGCTGGTMGATCGTCMGGCTTMGTCGCAMGGAATTCG-3'

The double-stranded oligonucleotide was labeled with
$^{32}$P-α-dCTP and Klenow enzyme. EMSA was conducted as
described previously (Durand et al., (1988) *Mol. Cell.*
*Biol.* 8:1715-1724). Briefly, binding of MED1 to
labeled oligonucleotides was carried out by incubating
1 µl out of 50 µl of the MED1 eluate, 7 X 10$^4$ cpm of
labeled oligonucleotides and 4 µg of poly (dI-dC) in
EMSA buffer (final volume of 20 µl) at room
temperature. Competition was carried out in the
presence of 100 ng (100-fold excess) of the cold
oligonucleotide. Binding reactions were separated on
a 6% non-denaturing polyacrylamide gel and visualized
by autoradiography of the dried gel.

For the electromobility shift assay employing the
purified methyl-CpG binding domain (MBD) of MED1, the
methylated probe was assembled by annealing the two
complementary oligonucleotides of Sequence I.D. No. 3
and Sequence I.D. No. 4. containing 5-methylcytosine.
See Figure 10B. The unmethylated probe was assembled
with two complementary oligonucleotides of identical
sequence to the oligonucleotides of Sequence I.D. No.
3 and Sequence I.D. No 4, except that cytosine
replaced 5-methylcytosine. Labeling of the probes was
conducted as above. DNA binding reactions were
carried out in 10 mM Tris-HCl pH 7.5, 50 mM NaCl, 5%
glycerol, 0.5 mM EDTA, 0.5 mM DTT, in the presence of
0.5 µg of polydA/polydT (ICN) as non-specific
competitor DNA [S. Buratowski and L.A. Chodosh, In
*Current Protocols in Molecular Biology,* eds. F. M.
Ausubel, *et al.,* John Wiley & Sons, New York (1996)].
Bacterially expressed and purified MBD (20 ng) was
incubated with the $^{32}$P-labeled double-strand
oligonucleotides (20,000 cpm, 0.2 ng) on ice for 30

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min.  For competition, the MBD was pre-incubated on
ice for 20 min with a 100-fold excess of the cold
oligonucleotide (20 ng) prior to addition of the
probe.  Binding reactions were loaded on a 10 %
acrylamide gel and run at 4°C in 0.5x TBE.  Dried gels
were exposed to autoradiography.

## H.  Co-immunoprecipitation analysis

To analyze the interaction of MED1 with hMSH2,
following transient transfection of 293 cells with the
constructs of the invention (Flag-tagged MED1), and
lysis of cells after a 72 hour period, proteins were
immunoprecipitated with anti-Flag antibody as
described above.  Immunoprecipitates were resuspended
in Laemmli buffer, boiled for 10 minutes, separated on
8.5% SDS-PAGE and transferred to Immobilon P
membranes.  Western blotting was carried out as
described above, using an antibody against hMSH2.

For analysis of the interaction of MED1 with
hMLH1, HEK-293 cells were cultured at 37°C and 7.5% $CO_2$
in Dulbecco's modified Eagle's minimum essential
medium (DMEM) supplemented with 10% fetal calf serum,
penicillin (50 units/ml), streptomycin (50 $\mu$g/ml), and
kanamycin (100 $\mu$g/ml).  Cells seeded in 100-mm Petri
dishes were transfected with the construct of the
invention, hemagglutinin-tagged MED1, using
LipofectAMINE (Life Technologies, Inc.) according to
the manufacturer's protocol.  Seventy-two hours later,
cells were lysed on ice in one of three lysis buffers,
containing 0.5% Nonidet P-40 (NP-40)[K. Datta et al.,
*Mol. Cell. Biol.* 15: 2304-2310 (1995)], 0.2% NP-40 [W.
Gu, K. Bhatia, I.T. Magrath, C.V. Dang, R.
Dalla-Favera, *Science* 264: 251-254 (1994)], or 1%
Triton X-100 [S. F. Law et al., *Mol. Cell. Biol.* 16:
3327-3337 (1996)]; NP-40 lysates were mildly sonicated

using a sonic dismembrator (Fisher).
Immunoprecipitations were carried out with the
anti-hemagglutinin tag antibody HA.11 coupled to beads
(Berkeley Antibody Company).   Immune complexes were
washed with lysis buffer, and the proteins were
resolved by 8.5% SDS-polyacrylamide gel
electrophoresis (SDS-PAGE) and transferred to PVDF
membranes (Immobilon P, Millipore) with an X-genie
electroblotter (Idea Scientific).   Membranes were
probed with an anti-MLH1 antibody (Pharmingen) and as
a control for expression of the construct, with the
HA.11 antibody (Berkeley Antibody Company).   Detection
of antigen-bound antibody was carried out using
enhanced chemiluminescence (ECL, Amersham), according
to the manufacturer's protocol.   See Figure 11C.


## I.   Expression of the MED1 catalytic domain in E. coli

The nucleic acid sequence encoding the catalytic
domain of MED1 was cloned in the vector pET28b
(Novagen) as a carboxyterminal fusion to a 6xHis tag
for expression in *E. coli*.   This construct was
transferred to the *E. coli* strain BL21(DE3)pLysS.
Overnight cultures were diluted 1:15 in fresh medium
and incubated for one-hour in a 37°C incubator.
Expression of the construct was induced by addition of
1 mM IPTG for an additional 3 hours at 37°C.   Cells
were then collected by centrifugation and lysed in
Laemmli buffer.   Lysates were boiled for 10 minutes
and separated on 12%  SDS-PAGE.   Proteins were
visualized by Coomassie blue staining.


## J.   Activity staining of the MED1-catalytic domain after *sodium dodecyl sulfate-polyacrylamide gel electrophoresis*

Activity staining of MED1 was performed

essentially as described by Blank et al. (Blank et al. (1982) Analytical Biochemistry 120: 267-275). Briefly, bacterial lysates expressing the MED1 catalytic domain were separated in SDS-polyacrylamide gels (12%) containing 0.15 mg/ml heat-denatured calf thymus DNA. Following electrophoresis, the gel was incubated in a buffer containing 10 mM Tris-HCl pH 7.4 and 25% isopropanol for one hour at room temperature with one change of buffer every twenty minutes. After the first hour, the gel was immersed in a buffer containing 10 mM Tris-HCl pH 7.4 for an additional hour with buffer changes every twenty minutes. The gel was then immersed in a buffer containing 10 mM Tris-HCl, pH 7.4, 10 mM $MgCl_2$, 5 mM $CaCl_2$, 2 µM $ZnCl_2$ for 16 hours at room temperature to allow digestion of DNA. DNA was visualized by staining the gel with 0.2% toluidine blue O in 10 mM Tris-HCl pH 7.4, followed by destaining in 10 mM Tris-HCl pH 7.4 for one hour at room temperature with one change of buffer every 20 minutes. Deoxyribonuclease activity results in a zone of clearing indicating reduced DNA staining (Blank et al., (1982) *supra*).

**K. Endonuclease activity of recombinant wild-type MED1.** The entire wild-type MED1 (codons 1-580, wt) and a deletion mutant lacking the endonuclease domain (codons 1-454, Δendo) were expressed in bacteria and purified by nickel-agarose chromatography. For bacterial expression, PCR-generated fragments corresponding to the entire MED1 open reading frame or to isolated domains were propagated in *E. coli* strain XL-1 Blue (Stratagene) and transferred into pET28(b) (Novagen). Constructs were sequenced with an automated DNA sequencer (ABI) to verify that unwanted mutations were not inadvertently introduced; and they

were transferred into *E. coli* strain BL21(DE3)pLysS.
These cells were grown to O.D.600= 0.4 and then
induced with 1 mM IPTG at 37°C for 3 hours.  Bacterial
lysates were purified over a nickel-agarose column
(Ni$^2$+-NTA agarose, Qiagen).  Increasing amounts of the
wild-type and Δendo mutant (22, 44, 87.5 and 175 ng)
were incubated with 500 ng of the 3.9 kb supercoiled
plasmid pCR2 (Invitrogen) at 37°C for 30 min in a
buffer containing 20 mM Tris-HCl pH 7.5, 25 mM KCl and
10 mM MgCl$_2$.  Reaction products were separated on a 1%
agarose gel buffered in 1x TAE and containing 0.25
µg/ml ethidium bromide.

## Identification and Characterization of MED1

To facilitate efforts to identify eukaryotic
functional homologues of the E. coli MutH
endonuclease, the yeast interaction trap assay, a
cloning strategy which screens for protein-protein
interactions in the yeast *S. cerevisiae* (Golemis et
al., 1996, supra) was employed.  This strategy was
based on the rationale that the human mismatch repair
endonuclease would interact with hMLH1, the human MutL
homologue, in a comparable way to what is observed in
bacteria where the endonuclease MutH interacts with
MutL.  The complete coding sequence of hMLH1 (amino
acids 1-756) was fused to the carboxy terminus of the
DNA binding domain of LexA.  This construct ("bait")
was introduced along with the appropriate reporter
plasmid in the yeast strain EGY191.  EGY191, which
harbors only two LexA operators directing
transcription of the chromosomal LEU2 gene, was used
because in initial experiments, employing the standard
EGY48 strain, the bait protein had constitutive
transcriptional activity (data not shown).  Western
blot analysis with an anti-LexA antibody showed that

pEG202-t-hMLH1 directs the synthesis of the expected size product for a LexA-hMLH1 bait protein in EGY191. In control experiments, performed following standard procedures, this protein was transported to the nucleus and did not activate transcription of the chromosomal LEU2 gene and of the episomal LacZ gene (data not shown). The EGY191/pSH18-34/pEG202-t-hMLH1 yeast cells were supertransformed with a human fetal brain cDNA library (approximately 4 x $10^5$ recombinants) fused to the B42 portable activation domain, and colonies growing on selective leucine-minus plates in the presence of galactose but not glucose as carbon source were isolated. Twenty-two clones (f1 to f22) were selected encoding putative hMLH1 interactors. One clone, designated f5, (later named MED1) was identified which strongly interacted with hMLH1, based on the early appearance of colonies on selective leucine-minus/galactose plates and on the intensity of color formation of colonies grown on indicator X-Gal/galactose plates. The specificity of the f5-hMLH1 interaction was assayed by supertransforming virgin EGY191/pSH18-34/pEG202-t-hMLH1 cells with f5 plasmid DNA. As a control, EGY191/pSH18-34 cells transformed with bait constructs of pEG202-bicoid, -MYC, -K-rev, and empty pEG202 vector, were also supertransformed with f5 DNA. Cells transformed with the combination of f5 and pEG202-t-hMLH1 grew on leucine-minus / galactose but not leucine-minus / glucose medium and turned blue on X-Gal / galactose but not X-Gal / glucose plates. Control cells failed to grow on leucine-minus / galactose and to turn blue on X-Gal / galactose plates, confirming specificity of the interaction between f5 and hMLH1 as shown in Figure 1.

Initial sequence analysis revealed that f5,

which was represented only once in this group of 22
putative interactors, codes for a protein sharing
homology with several bacterial endonucleases involved
in DNA repair.   Since the f5-encoded protein is a

5      putative DNA repair enzyme, its expression is expected
to be ubiquitous.   A Northern blot containing mRNA
from multiple tissues was probed with the entire 0.8
kb insert of the f5 clone. This analysis revealed
that, consistent with a putative housekeeping role in

10      DNA repair, the f5 gene is expressed in all normal
tissues tested with a transcript of approximately 2.4
kb.   See Figure 2.

In order to clone the remaining portion of the
gene, a f5-derived probe was used to screen four

15      additional cDNA libraries, three from fetal brain and
one from the  ovarian cancer cell line C200.   Six
clones were isolated from the fetal brain libraries
and 11 from the C200 library. These clones were
sequenced.   Overlapping sequences were aligned until

20      the nearly complete sequence of the gene was
determined (2.1 kb).   See Figure 3.   The MED1
transcript contains an open reading frame of 1740
bases, preceded by an in-frame stop codon, which
predicts a protein of about 580 amino acids encoded by

25      the sequence of Sequence I.D. No. 2.   Slight sequence
variations were observed between the cDNA clones
analyzed.   These are set forth below:

**SEQUENCE VARIATIONS**

1) Nucleotides 1325-1342:   18 nucleotides -

30      GTGAGAAAATATTTCAAG - are either present (as in
Sequence I.D. No. 1) or absent (as in Sequence I. D.
No. 23) from the cDNA, therefore the 6 amino acids
encoded by those nucleotides (GEKIFQ) are either
present (as in Sequence I. D. No. 2) or absent (as in

35      Sequence I. D. No.24) in the predicted protein.   This

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variation appears to originate from alternative usage
of a splice donor site. In the genomic DNA sequence:

...GACTTCACTG<u>GT</u>GAGAAAATATTTCAAG**GT**...

If the second splice donor site (bold) is used,
then the 18 nucleotides GTGAGAAAATATTTCAAG are
incorporated in the mRNA; if the first splice donor
site (underlined) is used, then the same 18
nucleotides are spliced out and are not incorporated
in the mRNA.

2) Nucleotide 1876: T (as in Sequence I.D. No. 1) or C
(as in Sequence I. D. No. 25), therefore codon 579 is
either TTA or CTA (no amino acid variation, since both
code for leucine).

3) Nucleotide 2042: C (as in Sequence I.D. No. 1) or T
(as in Sequence I. No. 26), (no amino acid variation,
since this change is in the 3' untranslated region).

4) Poly-A tail:  Added after nucleotide 2106 (as in
Sequence I.D. No. 1) or approximately 150-200 bases
downstream (precise site not determined): this
variation probably originates from an alternative
polyadenylation signal.

5)  Nucleotide 1214 = T (as in Sequence I.D. No. 1) or
C (as in Sequence I. D. No. 27), therefore codon 358
is either ATC or ACC, coding for isoleucine or
threonine, respectively.  This sequence variation is
described in more detail in relation to Example II.

Analysis of the predicted MED1 protein sequence
reveals a tripartite structure.  At the amino
terminus, MED1 contains a region of homology to the
methyl-CpG binding domain (MBD) of MeCP2, a
chromosomal protein which binds CpG-methylated DNA and

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may mediate the effects of DNA methylation on chromatin structure and transcription (Lewis et al., (1990) *Cell* 69:905-914; Nan et al., (1993) *Nucleic Acids Res.* 21:4886-4892). The same region of MED1 is

5    also homologous to the MBD of the human protein PCM1, a component of the transcriptional repressor MeCP1 (Cross et al., (1997) Nat. Genet. 16:256-259). The central portion of MED1 does not display a recognizable domain structure, but it appears to be

10   rich in positively-charged amino acids, often arranged in short clusters which might represent nuclear localization signals (Boulikas, T., (1993) *Critical Rev. in Eukaryotic Gene Expression* 3:193-227). Finally, at the carboxy terminus, MED1 contains a

15   putative catalytic domain sharing homology with several bacterial endonucleases of the glycosylase/lyase type involved in DNA repair, including MutY and endonuclease III from *E. coli*, ultraviolet endonuclease from *Micrococcus luteus*, and

20   the putative endonuclease encoded by the ORF10 of the thermophilic archaeon *Methanobacterium thermoformicicum*. See Figure 4A, 4B and 4C. A schematic of the domain organization of MED1 is shown in Figure 5.

25       In order to confirm that the MED1 open reading frame is capable of directing the synthesis of a protein product, a construct of MED1 in the vector pcDNA3 was employed in an *in vitro* coupled transcription and translation assay. The result

30   indicated that the MED1 open reading frame drives the translation of two polypeptides of 70 and 65 kD, shown in Figure 6, in good agreement with the molecular weight predicted from the amino acid sequence. The synthesis of these two polypeptides might be the

35   result of initiation from the two close ATG codons, at

nucleotide position 142 and 262, respectively. Such a possibility is known to occur as a result of "leaky" ribosome scanning and is increased by a suboptimal Kozak's context (Kozak, M., (1995) *Proc. Natl. Acad. Sci.* 92:2662-2666). The difference in molecular weight (5kD) would be compatible with the distance between the two ATG codons (40 a.a.). To determine if two MED1 proteins are also synthesized *in vivo*, a hemagglutinin epitope was fused at the carboxyterminal end of the MED1 open reading frame, generating the construct MED1-HT. Constructs were also generated which fused a hemagglutinin tag immediately before each of the two putative initiation codons (HT-MED1-M1 and HT-MED1-M2). These constructs were transiently transfected in NIH-3T3 cells and lysates of the transfectants were prepared and separated by SDS-PAGE. Western analysis with an anti-hemagglutinin tag antibody revealed the presence of a band of approximately 72 kD in cells transfected with the carboxyterminally tagged MED1-HT. This band comigrates with the one present in HT-MED1-M1 transfectants, indicating that the first ATG at nucleotide position 142 is the initiation codon *in vivo*. See Figure 7. Since the expression level of HT-MED1-M1 which uses the hemagglutinin tag ATG codon is much higher than MED1-HT which uses the autologous ATG codon, it is possible that the expression of the MED1 protein is under a tight translational control.

Finally, the MED1 gene was mapped with fluorescence in situ hybridization to human chromosome 3q21-22. See Figure 8.

In order to determine whether MED1 has endonuclease activity, the catalytic (endonuclease) domain was expressed in *E. coli* as a carboxyterminal fusion to a 6xHis tag. High levels of expression of

the domain as a polypeptide of approximately 18-22 kD were achieved.  See Figure 9A, left panel.  Bacterial lysates expressing the catalytic domain were separated in an activity polyacrylamide gel containing denatured calf thymus DNA.  Following electrophoresis, the gel was incubated in a Tris-buffered solution containing 25% isopropanol and then in Tris buffer alone to allow digestion of DNA.  DNA was visualized by staining the gel with toluidine blue O.  Results revealed a zone of clearing, indicative of DNA digestion, migrating at approximately 18-22 kD in *E. coli* lysates expressing the endonuclease domain but not in control lysates.  See Figure 9A, right panel.  This experiment indicates that the recombinant catalytic domain of MED1 displays deoxyribonuclease activity.

To better define its nuclease properties, the entire MED1 protein was expressed in *E. coli* as a carboxyterminal fusion to a six-histidine tag and purified on a nickel-agarose column to approximately 95% homogeneity.  See Figure 9B, left panel. Endonuclease activity was assayed by evaluating the conversion of a supercoiled plasmid into open circles (nicked) and linear molecules.  Increasing amounts of the purified MED1 protein were incubated with supercoiled plasmid DNA at 37°C for 30 min, and the products of the reactions, separated on a 1% agarose gel, were visualized by ethidium bromide staining. Incubation with MED1 resulted in a dose-dependent appearance of nicked and linearized molecules (Fig. 9B, right panel).  In order to rule out the possibility that a bacterial endonuclease activity copurifying with MED1 is responsible for the observed effects, a deletion mutant lacking the putative endonuclease domain was also purified.  This mutant failed to produce nicked and linearized DNA molecules

(Fig. 9B, right panel). These results indicate that
MED1 has single- and double-strand endonuclease
activity on a supercoiled plasmid substrate.
Additional studies of the catalytic activity of MED1
are presented in Example V.

Digestion of the MED1-linearized plasmid with the
restriction enzyme EcoRI, which performs two closely
spaced cuts on this plasmid, resulted.in the
appearance of a smear, indicating that MED1 does not
have preferential cutting sites on this substrate.
The production of linear molecules by MED1 in the
above assay is intriguing. The kinetics suggest rapid
counter-nicking of the second strand across from a
site where the first nick is formed. It will be
interesting to determine whether the MED1 nicks occur
in CpG-rich regions and whether cytosine methylation
modulates the second nicking event.

To assess whether the MED1 methyl-CpG binding
domain (MBD) is able to bind methylated DNA, a FLAG
epitope was fused at the amino terminal end of the
MED1 open reading frame, generating the construct FT-
MED1/f5, and this construct was transfected into the
human kidney line 293. Cells were also transfected
with the empty expression vector. Seventy-two hours
after transfection, cells were lysed and the lysates
were immunoprecipitated with an anti-Flag antibody
coupled to agarose beads. Bound protein was eluted
from the beads following incubation with a FLAG
peptide. The FT-MED1/f5 and control eluates were
incubated with a $^{32}$P-labeled double-stranded
oligonucleotide containing a total of five fully
methylated CpG sites, in the presence or absence of a
100-fold excess of the unlabeled or "cold"
oligonucleotide. The binding reactions were separated
on a non-denaturing polyacrylamide gel and detected by

autoradiography of the dried gel.  A slowly migrating
band was detected in the FT-MED1/f5 eluate lanes, but
not in the control lane.  This band was abolished by
competition with excess cold oligonucleotide.  This
experiment indicated that the MBD of MED1 functions as
a specific methylated DNA binding domain in vivo.  See
Figure 10A.

To further characterize the DNA binding
properties of MED1, its putative methyl-CpG binding
domain (MBD) was expressed in *E. coli* as a
carboxyterminal fusion to a six-histidine tag, and it
was purified by metal-chelating affinity
chromatography followed by ion-exchange chromatography
on SP Sepharose (Pharmacia).  The purity of the MED1
MBD was estimated at >98% by SDS-PAGE followed by
Coomassie staining.  The purified MBD was incubated
with a $^{32}$P-labeled double-strand oligonucleotide of
arbitrary sequence containing five symmetrical
methyl-CpG sites.  As a control, MBD was incubated
with a $^{32}$P-labeled double-strand oligonucleotide of
identical sequence in which cytosines replaced 5-
methyl-cytosines.  EMSA analysis of the complexes
indicated that the MED1 MBD binds to methylated DNA
and fails to bind to unmethylated DNA (Fig. 10B, lanes
2 and 6).  Binding to the methylated probe was
competed by preincubation with a 100-fold excess of
cold methylated oligonucleotide (lane 3).  Little
competition was observed following preincubation with
the unmethylated oligonucleotide (Fig. 10B, lane 4).
This experiment provides further evidence of the
methyl-CpG binding specificity of the MED1 MBD.

The physical association of MED1 with other DNA
repair proteins was assessed as follows.  293 cells
were transfected with the construct FT-MED1/f5 or with
an empty expression vector.  Seventy-two hours after

transfection, cell lysates were prepared and immunoprecipitations carried out with anti-FLAG antibodies coupled to agarose beads. Immunoprecipitated proteins were separated by SDS-

5      PAGE, transferred to membrane and probed with anti-hMSH2 antibody.  The antibody detected a band of approximately 103 kD comigrating with hMSH2 in the anti-FLAG immunoprecipitate from FT-MED1/f5 tranfected 293 cells but not from control cells.  See Figures 11A

10     and 11B.  This experiment demonstrates the physical association of MED1 in a complex with hMSH2.

In order to confirm that the hMLH1 / MED1 interaction detected in yeast also occurs in human cells, co-immunoprecipitation experiments were

15     performed.  Human kidney HEK-293 cells were transfected with a hemagglutinin-tagged construct of MED1 (HT-MED1) or with an empty expression vector. Seventy-two hours after transfection, cell lysates were prepared and immunoprecipitations were carried

20     out with an antibody directed against the hemagglutinin tag.  Immunoprecipitated proteins were separated by SDS-PAGE, transferred to a membrane and probed with an anti-MLH1 monoclonal antibody.  The antibody detected a band of approximately 82 kD

25     co-migrating with MLH1 in the anti-hemagglutinin immunoprecipitate from HT-MED1-transfected HEK-293 cells but not from control cells (Fig. 11C).  This experiment suggests that MED1 is present in a complex with MLH1.

30                              **EXAMPLE II**

**Identification of Mutations in MED1 in HNPCC patients**

Mutational screening of the MED1 gene has been performed in ten HNPCC patients.  Earlier studies on these patients revealed that they were negative for

35     hMSH2 and hMLH1 mutations (Viel et al., (1997) Genes

Chromosom Cancer 18:8-18). Polymerase chain reaction
(PCR) amplification of MED1 fragments with MED1-
specific primer oligonucleotides (provided in Table
I), has been performed followed by direct sequencing
of PCR products. A sequence variant which converts
isoleucine 358 to threonine (I358T) has been
identified in the germ-line of a female patient
affected by two independent synchronous colon cancers.
Analysis of one of the cancers revealed the loss of a
normal allele. This finding is in agreement with a
possible tumor suppressor role of MED1. The I358T
variant is presently being searched in other affected
and unaffected individuals of the family to determine
if it cosegregates with the disease. Thus, the I358T
variant is present at a frequency of 1 out of 10 HNPCC
patients (10%). This variant is also present in the
general population at a lower frequency of
approximately 3 out of 69 individuals (4.3%). Taken
together these findings suggest that the I358T variant
of MED1 may be associated with an increased risk for
colon cancer. Additional MED1 sequence variants are
being analyzed in families predisposed to cancer.


**EXAMPLE III**

**Screening Cancer Patient DNA Samples**

**for Mutations in MED1**

A panel of 14 sporadic colorectal cancers with
microsatellite instability but with no detectable
defect in the two major mismatch repair genes, hMSH2
and hMLH1 (Y. Wu et al *Genes Chromosomes and Cancer*
18, 269: 1997) were screened for mutations by PCR
amplification of all the MED1 exons from genomic DNA,
followed by direct sequencing of PCR products with an
automated DNA sequencer (ABI), using the primers shown
in Table I. Some of these cancers exhibited loss of

expression of MLH1.

Sequence analysis revealed MED1 mutations in 4 of 14 (28.6%) tumors. In all four of these tumors, a one-base deletion occurred in one of two mononucleotide repeats [(A)6 and (A)10] located in the coding region of MED1 (Fig. 12A and 12B) (Mutations were confirmed by sequencing at least three independent PCR products on both strands); the mutations were somatic, as they were not detected in the corresponding peripheral blood DNA. The one-base deletions cause frameshifts and predict the synthesis of truncated proteins (Fig. 12C). These alterations resemble the frameshift mutations described in the (A)8 and (C)8 tracks present in the coding region of the mismatch repair genes MSH3 and MSH6, respectively (S. Malkhosyan et al *Nature* 382:499, 1996). Furthermore, these alterations appear to be selected for in tumor cells, as similar (A)n mononucleotide repeats, including the (A)8 stretch in the coding region of PMS2, are not altered in this tumor panel. Similarly, preliminary screening experiments of 26 endometrial cancer patients led to the identification of a mutation in MED1.

**TABLE II**

| Patient | Sex | Tumor Site | Age at Diagnosis | MED1 Mutation | MED1 Codon | Result |
|---------|-----|------------|------------------|---------------|------------|--------|
| c18T | F | caecum | 83 | (A)10 to (A)9 | 310-313 | frameshift and stop at codon 317 |
| C220T | M | traverse colon | 79 | (A)10 to (A)9 | 310-313 | same as above |
| c226T | F | ascending colon | 70 | (A)10 to (A)9 | 310-313 | same as above |
| c215T | F | caecum | 66 | (A)6 to (A)5 | 280-282 | frameshift and stop at codon 317 |
| UPN252T | F | endometrium | N/A | (A)10 to (A)9 | 310-313 | frameshift and stop at codon 317 |

## Discussion

Two long-standing and closely related issues in eukaryotic mismatch DNA repair are identifying the endonuclease activity responsible for incising the DNA strand carrying the mutation, and defining the nature of the strand-targeting signal. In *E. coli*, MutH performs this function through the recognition of hemimethylated d(GATC) sites. However, eukaryotic functional homologues of MutH are not currently known. Due to the lack of information on the molecular determinants of strandedness, it was hypothesized that a reasonable approach towards the cloning of eukaryotic MutH functional homologues would be to identify hMLH1 interactors. By analogy with the MutL-MutH interaction in the bacterial system, the eukaryotic mismatch repair endonuclease is expected to be a hMLH1 interactor.

Accordingly, the "interaction cloning" of MED1, a gene encoding a viable candidate for a mismatch repair protein is described in the previous examples. The MED1 protein has several features compatible with such a role. MED1 specifically interacts with hMLH1 in the yeast system and mammalian cells, and with hMSH2 in a mammalian cell system. Whether MED1 interacts with other components of the mismatch repair complex, such as hMSH3, hMSH6/GTBP and hPMS2 has yet to be determined. MED1 has a catalytic domain showing homology to several bacterial DNA repair endonucleases, and based on this homology, it is predicted that MED1 would have N-glycosylase and possibly apurinic or apyrimidinic (AP) lyase activities. As shown in the following examples, MED-1 is a mismatch specific glycosylase, yet does not appear to possess lyase activity. Among the MED1 homologues, both the *E. coli* MutY and endonuclease III, and the *M. luteus* UV-repair endonuclease have DNA N-glycosylase and AP lyase activities. Interestingly, MutY is active on A.C,

A.G and A.8-oxoG mismatches, whereas endonuclease III is
active on mismatches containing some damaged derivatives
of thymidine and cytosine. The homology between MED1 and
the ORF10-encoded protein of *M. thermoformicicum*
(Nolling et al., (1992) *Nucleic Acids Res.* 20:6501-6507)
is particularly intriguing. It has been proposed that
this open reading frame encodes a mismatch DNA repair
enzyme, functionally associated with the methylase of the
*M. thermoformicicum* restriction/modification system.
ORF10 would be active on G/T mismatches originated by
deamination of 5-methyl-cytosine, a product of the
methylase, to thymidine under thermophilic conditions.
Spontaneous deamination of 5-methyl-cytosine in CpG
dinucleotides to thymidine (G.m5C → G.T) is a source of
endogenous mutations in the human genome (Rideout et al.,
(1990) *Science* 249:1288-1290). Almost 50% of the p53
point mutations in colorectal cancer are transitions at
CpG dinucleotides (Greenblatt et al., (1994) *Cancer Res.*
54:4855-4878). Conservation of MED1-related sequences
involved in mismatch repair in organisms belonging to two
distant phyla (Eubacteria and Archeobacteria) suggests
that human MED1 is an enzyme active on DNA mispairs.

A common feature of the MED1-related endonucleases
is the presence of a Cys-X6-Cys-X2-Cys-X5-Cys sequence at
their carboxy terminus. This sequence, as shown in
endonuclease III, ligates the [4Fe-4S] iron-sulfur
cluster and defines a novel DNA binding motif (named the
FCL motif), which provides the correct alignment of the
enzyme along the DNA (Thayer et al., (1995) Embo J.
14:4108-4120). MED1 lacks a FCL motif at its carboxy
terminus, but contains a methyl-CpG DNA binding domain at
the amino terminus.

The interpretation of the MED1 mutational data
requires some caution. Although it is presently unclear
whether MED1 mutations promote or are the consequence of

microsatellite instability, their apparent selection in
tumors suggest that they may contribute to the unfolding
of tumor genomic instability, as has been proposed for
the *MSH3* and *MSH6* coding microsatellite mutations (M.

5      Perucho, *Nature Med* 2: 630-631, 1996). Due to the
variable amount of contaminating normal cells in primary
tumor specimens, it is difficult to determine the
homozygous or heterozygous nature of the MED1 mutations.
Sequence analysis (Fig. 12) shows apparent retention in

10     the tumors of the wild-type MED1 allele, however more
extensive studies have revealed a loss of heterozygosity
in this region. This may indicate that the products of
the mutant alleles, which lack the catalytic domain (Fig.
12C), act in a dominant negative fashion, perhaps

15     competing for methyl-CpG DNA binding. Alternatively, the
heterozygous mutations may reduce the total amount of
functional molecules (haploinsufficiency).

        Like other mismatch repair genes which are mutated
in HNPCC as well as in sporadic cancers with

20     microsatellite instability, MED1 is a candidate gene for
cancer genetic testing, both in HNPCC families and in
sporadic cancers with microsatellite instability. It
should be noted that only about 70% of HNPCC cases and
only about 65% of sporadic tumors with microsatellite

25     instability carry mutations in the known mismatch repair
genes hMSH2, hMLH1, hMSH6, hPMS2 and hPMS1. The remainder
30-35% of the cases have an as yet unidentified mismatch
repair defect and a fraction may therefore harbor
mutations or loss of expression of MED1. Indeed,

30     frameshift MED1 mutations were detected in both
colorectal and endometrial cancers. See Figure 12 and
Table II.

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## EXAMPLE IV

**Single-strand conformation polymorphism (SSCP) analysis**
**of MED1 mutations and LOH analysis at the MED1 locus.**

As mentioned in the previous examples, mutations
in MED1 encoding nucleic acids have been identified in
patient tumor samples. The present example describes two
approaches for identifying and characterizing MED1
mutations in patient DNA.

SSCP analysis was performed by PCR amplification of
two MED1 segments encompassing the coding microsatellite
repeat regions poly(A)$_{10}$ and poly(A)$_6$. In particular, PCR
reactions were carried out with the MED1 primers 5'-
CTCGTTGTGTTCTGAGCTTTTGGC-3' (SEQ ID NO: 30) and 5'-
CAGTGTGACCAGTGAAGAAAA-3' (SEQ ID NO: 31) for analysis of
the (A)$_{10}$ repeat at codons 310-313; and 5'-
TGAAAGGAATCCCAATTAAG-3' (SEQ ID NO: 32) and 5'-
GACAGTTCTATCAAGCTGAC-3' (SEQ ID NO: 33) for analysis of
the (A)$_6$ repeat at codons 247-248.

PCR reactions were carried out in a volume of 20 µl
containing: 50 ng of genomic DNA, 1.5 mM MgCl$_2$, 50 mM KCl,
10mM Tris-HCl pH 8.3, 200 µM each of dATP, dGTP, dTTP, 40
µM dCTP, 0.1µCi of α-$^{32}$P dCTP (NEN-DUPONT), 1µM each
primer and 0.5 U of Taq Polymerase (Perkin Elmer/Cetus).
Amplification was conducted in a MJ Research PTC 200
thermocycler for 35 cycles. Each cycle consisted of 1
min at 94 °C, 1 min at 58 °C and 1 min at 72 °C, followed
by a 5-min extension at 72 °C. After the PCR reaction, a
2 µl aliquot of the product was diluted into 20 µl of
denaturing loading buffer (98% formamide, 10mM EDTA, pH
8.0, 0.25% xylene cyanol FF, and 25% bromophenol blue),
heated at 95 °C for 5 min and cooled on ice for 5 min. 3
µl of this solution were loaded on SSCP gels for
electrophoretic separation.

SSCP gels consisted of 0.6 x MDE solution (FMC
BioProducts, Rockland, ME, USA) and 0.6 x TBE buffer and

were run in 0.6 x TBE buffer at 6 W for 12-14 hrs at room
temperature. Following electrophoresis, gels were dried
and exposed to autoradiography film (X-OMAT, Kodak)
overnight at room temperature.

5      PCR conditions for loss of heterozygosity (LOH)
analysis of markers (Research Genetics) were identical to
those for SSCP.  PCR products were analyzed on 6%
polyacrylamide gels and visualized by auto-radiography.

**RESULTS**

10      A common theme in tumors with microsatellite
instability (MSI) is the presence of frameshift mutations
in microsatellites located in the coding region of target
genes.  Thus, the transforming growth factor β type II
receptor gene (*TGFBR2*) is frequently inactivated in MSI-
15     positive colorectal and gastric carcinomas, due to
deletions or insertions in a coding $(A)_{10}$ track. The
insulin-like growth factor II receptor gene (*IGF2R*) and
the proapoptotic gene *BAX* are inactivated by mutations in
coding $(G)_8$ tracks.  Additional target genes in tumors
20     with MSI, are the β2-microglobulin gene (*B2M*) and the
tumor suppressor gene, *PTEN*.  Interestingly, two DNA
mismatch repair (MMR) genes, *MSH3* and *MSH6*, are often
somatically mutated in MSI tumors at coding $(A)_8$ and $(C)_8$
tracks, respectively.  In the latter case, it has been
25     proposed that the genomic instability develops gradually,
as an initial mutation in a primary MMR gene (*MSH2* or
*MLH1*) leads to secondary MMR gene mutations, further
impairing MMR functions.

Inspection of the *MED1* coding sequence highlighted
30     four potential hypermutable tracks: one $(A)_{10}$ track at
codons 310-313 and three $(A)_6$ sequences at codons 247-248,
280-282, and 327-329.  We screened a panel of both MSI
and microsatellite-stable (MSS) primary tumors and cell
lines for mutations in these polyadenine tracks by
35     polymerase chain reaction (PCR), followed by single-

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strand conformational polymorphism (SSCP) analysis and direct sequencing. In addition, we cloned PCR products and obtained the sequence of multiple clones, thus allowing biochemical characterization of the mutations.

We detected *MED1* mutations in 14 of 56 (25%) primary MSI tumors. Specifically, mutations were demonstrated in 11 of 42 (26.2%) colorectal carcinomas, 2 of 9 (22.2%) endometrial carcinomas and 1 of 5 (20%) pancreatic tumors (Figs. 20A, 20B). Analysis of the corresponding normal DNAs indicated that the mutations are somatic (Figs. 20A, 20B). None of 116 MSS tumors (39 colorectal, 36 endometrial and 41 pancreatic tumors) contained *MED1* mutations at these coding polyadenine tracks, suggesting that mutations at these tracks are restricted to MSI tumors ($P< 5 \times 10^{-6}$, Fisher's exact test). Similarly, we detected a *MED1* mutation in 1 of 6 MSI cell lines (HCT116, Fig. 20A) and in none of 8 MSS cell lines (Fig. 20A). All of the mutations identified, with one exception, targeted the $(A)_{10}$ track; the exception was a mutation targeting the $(A)_6$ track at codons 247-248 (Table III). This result indicates that the $(A)_{10}$ track is a mutational hotspot in *MED1*. All the mutations consisted of one- or two-basepair deletions or one-basepair insertion, thus causing frameshifts and premature stop codons. The resulting truncated proteins are predicted to be non-functional, as they would lack the carboxyterminal catalytic domain, located at codons 455-580. The frameshift mutations in *MED1* appear to be selected for in MSI tumor cells, as similar coding polyadenine repeats in other tested genes are rarely altered in this panel of 56 primary MSI tumors; specifically, we detected no mutation in the $(A)_8$ track of the *PMS2* MMR gene, and found only two mutations in the $(A)_9$ track of the DNA helicase genes, *BLM* and *RECQL* ($P=0.00122$, 0.00183 and 0.00418, respectively; McNemar's

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test).

The presence of normal cells in primary tumor
specimens (Table III) makes it difficult to determine the
homozygous or heterozygous nature of *MED1* mutations by
5    SSCP and DNA sequencing.  For this reason, we conducted
loss of heterozygosity (LOH) studies on 6 of the 11
colorectal carcinomas with *MED1* mutations for which
sufficient amounts of matched normal and tumor DNAs were
available.  First, by screening the GeneMap database, we
10   localized *MED1* to a 0.4-Mb interval defined by markers
*D3S3606* and *D3S1587*.  This map position confirmed our
FISH data localizing *MED1* to 3q21-22.  See Figure 8.  We
then performed LOH analysis using these two
microsatellite markers and 9 other closely linked
15   polymorphic markers derived from the Genetic Location
Database (LDB) map.  Thus, the following markers were
used: *D3S1589, D3S3584, D3S2316, D3S3606, D3S1587,*
*D3S1290, D3S1292, D3S3657, D3S1664, D3S1615, D3S3554.*
Three tumors exhibited interstitial losses involving
20   3q21.3-22.1.  The borders of the interstitial deletions
were defined by the markers *D3S3584* and *D3S1664* (Fig. 20C
and 20D).  Two dozen genes map to this 3.1-Mb region,
with *MED1* being the only obvious gene proposed to be
involved in oncogenesis.  Colorectal tumor c698T
25   displayed no evidence of LOH, in agreement with its
unique SSCP pattern (Fig. 20A) and DNA sequencing
analysis, which indicated two different somatic
mutations, an $(A)_9$ and an $(A)_8$ sequence at codons 310-313
(Table III).  Thus, 4 of these 6 colorectal tumors had
30   evidence of biallelic inactivation of *MED1*.
These studies indicate that LOH analysis with the above-
mentioned markers (*D3S1589, D3S3584, D3S2316, D3S3606,*
*D3S1587, D3S1290, D3S1292, D3S3657, D3S1664, D3S1615,*
*D3S3554*) provides a means to initially screen tumors for

mutations in MED1.  It is possible that cancer specimens without MED1 genetic mutation might exhibit loss of MED1 protein expression by other mechanisms, including promoter hypermethylation.

5        In colorectal tumors, the frequency of *MED1* mutations was similar in HNPCC tumors associated with a known *MSH2/MLH1* germline mutation (6 of 21, 28.6%) and in sporadic tumors lacking *MSH2/MLH1* mutation but displaying loss of MLH1 or MSH2 expression by immunohistochemistry

10    (5 of 21, 23.8%)(Table III).  This indicates that *MED1* is a frequent target of the genomic instability in MSI colorectal carcinomas regardless of their hereditary or sporadic origin.  With regard to its proposed role in regulating genomic stability, *MED1* alterations may

15    represent "mutator's mutations" that contribute to the progressive unfolding of genomic instability in these tumors, as has been suggested for *MSH3* and *MSH6* frameshift mutations.

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## Table III

## Pathological and molecular features of MSI tumors
## carrying *MED1* mutations

| Sample | Tissue Type | *MLH1/MSH2* Mutation | Histopatho- logical Grade | Clinical Stage | % Tumor Cells | Codon |
|---|---|---|---|---|---|---|
| c18 | sporadic colon | none[a] | 3 | I | 90 | 310-31 |
| c215 | sporadic colon | none[a] | 2 | III | 95 | 247-24 |
| c220 | sporadic colon | none[b] | 2 | II | 15 | 310-31 |
| c226 | sporadic colon | none[a] | 3 | III | 90 | 310-31 |
| c493 | sporadic colon | none[a] | 1 | II | 75 | 310-31 |
| c35 | HNPCC | *MLH1* exon 16 | 1 | III | 60 | 310-31 |
| c219 | HNPCC | *MLH1* exon 17 | 3 | II | 90 | 310-31 |
| c587 | HNPCC | *MLH1* exons 3-5 | 2 | II | 65 | 310-31 |
| c698 | HNPCC | *MLH1* exon 16 | 2 | I | 70 | 310-31 310-31 |
| c1027 | HNPCC | *MLH1* exon 16 | 2 | II | 65 | 310-31 |
| c1077 | HNPCC | *MLH1* exon 16 | 2 | II | 65 | 310-31 |
| e4 | sporadic endometrial | ND | 3 | NA | 50 | 310-31 |
| e252 | sporadic endometrial | ND | NA | NA | NA | 310-31 |
| p108 | sporadic pancreas | ND | 2 | II | 70 | 310-31 |

[a]Loss of MLH1 and [b]loss of MSH2 expression by immunohistochemistry.
Grade 1: well differentiated; 2: moderately differentiated;
3: poorly differentiated. Staging of colorectal and pancreatic
carcinomas is according to TNM staging system. Percent tumour cells
in specimens was estimated by light microscopy of paraffin-embedded
sections. Del: deletion; ins: insertion. ND: not done; NA: not
available.

## EXAMPLE V

## G:T mismatch specific glycoslyase activity of MED1

The enzymatic activities of MED1 have been further
characterized. In accordance with the present invention,
it has been determined that MED1 is a G:T mismatch

specific glycoslyase.

The following methods are provided to facilitate the
practice of Example V.

**Preparation of the oligonucleotide substrates.**

The enzymatic activity of the entire MED1 protein
and the catalytic domain was analyzed using as substrate
64- or 37-mer double-strand oligonucleotides set forth
immediately below, containing several mismatches
including insertions and a deletion  The oligos were
synthesized on an Applied Biosystems DNA synthesizer and
purified by denaturing 15-20% PAGE - 8.3M urea gel
followed by DNA electroelution from the gel slices using
an Amicon 57005 electroeluter.

The annealed oligonucleotides were obtained by
mixing equal amounts of single-strand oligonucleotides in
10 mM Tris pH 7,5, 10 mM MgCl$_2$, 1mM DTT, 50mM NaCl,
heating the mix at 80°C for 15 min and then allowing the
mix to slowly cool to room temperature. The labeling
consisted of a fill-in reaction with the DNA polymerase
enzyme Prime-It (Stratagene) at the 3' end of the bottom
strand using $\alpha^{32}$P-dGTP in the same annealing buffer.

```
5' CCGTCATGCTAGTTCACTTTATGCTTCCGGCTCXCGTCATGTGTGGAATTGTGATTAAAATCG   3'
3'  GCAGTACGATCAAGTGAAATACGAAGGCCGAGYGCAGTACACACCTTAACACTAATTTTAGCG   5'
```

**X**= A,G,C,T
**Y**= A,G,C,T,U,E

```
5' CCGTCATGCTAGTTCACTTTATGCTTCCGGCTZGCGTCATGTGTGGAATTGTGATTAAAATCG   3'
3'  GCAGTACGATCAAGTGAAATACGAAGGCCGAWJGCAGTACACACCTTAACACTAATTTTAGCG   5'
```

**Z:W**= A:T,G:C,C:G,T:A
**J**= T,U

K

```
5' CCGTCATGCTAGTTCACTTTATGCTTCCGGCTCG^CGTCATGTGTGGAATTGTGATTAAAATCG   3'
3'  GCAGTACGATCAAGTGAAATACGAAGGCCGAGC.GCAGTACACACCTTAACACTAATTTTAGCG   5'
```

**K**= Ins A,G,C,T,GT,GTA,GTAC,GTACT,GGGGG;  del C

```
5' CAATCCTAGCTGACACGATGTGGCCAATGGCATGACT   3'
3'  TTAGGATCGACTGTG@TACACCGGTTACCGTACTGAG   5'
```

@= C,T,U,E
G= Guanine, C= Cytosine, T= Thymine, A= Adenine, U= Uracyl, E= etheno
Cytosine

## Glycosylase Assay

For the glycosylase assay, a 15 µl reaction containing 5nM of 3' end labeled oligo and 5 nM of recombinant MED1 was incubated at 37°C for 1 hour in 20mM Hepes, pH 7.5, 1 mM EDTA pH 8, 1 mM DTT, 0.1 mg/ml bovine serum albumin. Fifty percent of the reaction was treated with 100 mM NaOH at 90°C for 30 min. Formamide loading buffer (95% formamide, 0.04% bromophenol blue and xylene cyanol, 20 mM EDTA and 10 mM NaOH) was added to the NaOH-treated samples and the reactions were loaded on a 15% PAGE – 8.3M Urea gel in order to separate the product from the substrate. Gels were exposed to autoradiography. A schematic of this assay is shown in Fig. 21.

## RESULTS

### Glycosylase Activity of MED1

As mentioned previously, the catalytic domain of MED1 bears distant homology to several bacterial DNA repair glycosylases/lyases, including MutY and endonuclease III from *E. coli*, Mig.*Mth* or (previously referred to as ORF10) from *M. thermoautotrophicum*, and UV endonuclease from M. luteus. See Figure 4B . Whereas endonuclease III and the closely related UV endonuclease have both N-glycosylase and apurinic-apyrimidinic (AP) – lyase activity, and are active on thymine residues damaged by ring saturation, fragmentation or contraction, MutY and Mig. Mth are mismatch specific N-glycosylases. MutY is an adenine glycosylase, and possibly AP – lyase, active on A:C and A:G mismatches as well as on adenine paired with 8-oxo-guanine. Mig.*Mth* from the thermophilic archeon *M. thermoautotrophicum* is a thymine glycosylase

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active on G:T mismatches; the enzyme is equally active on G:U and to a less degree on G:G, A:G, T:C and U:C mismatches.

Based on the observed homology with these enzymes, MED1 was assayed for glycosylase activity on mismatched bases. A schematic of the glycosylase assay is shown in Figure 21. Purified recombinant MED1 protein was incubated with $^{32}$P-labelled oligonucleotide substrates carrying all the 8 possible mismatches of the normal DNA bases. The products of the reaction were treated with strong alkali to cleave at AP sites and then were separated by electrophoresis on denaturing polyacrylamide gels. As shown in Fig. 22, a cleavage product was detected on the $^{32}$P-labeled, thymine-containing strand of a G:T substrate. A sequencing ladder indicated that the migration of the cleavage product corresponds to the site of the mismatched thymine (data not shown). No cleavage was detected on C:T or T:T mismatches (Fig. 22). In addition, no cleavage product was detected when MED1 was incubated with matched oligonucleotide substrates (Fig. 21) or with substrates containing 1 to 5 extrahelical bases. These results indicate that MED1 has thymine glycosylase activity specific for G:T mismatches.

## MED1 lacks a detectable lyase activity

In addition to the glycosylase activity, endonuclease III and UV-endonuclease perform a β-elimination reaction of the AP site with their associated AP lyase activity (bifunctional glycosylases/lyases). In order to determine whether MED1 has AP lyase activity, fractions from the last step of purification of recombinant MED1 (gel filtration) were incubated with the $^{32}$P-labeled G:T substrate. Following incubation with MED1, an aliquot of the reaction was processed with NaOH before electrophoresis, whereas the remaining directly

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underwent electrophoresis.  As shown in Fig. 23, no
cleavage was detected when the incubation of the MED1
reaction products with alkali was omitted.  This
indicates that MED1 is a monofunctional glycosylase that
5     lacks a detectable lyase activity.


## MED1 thymine glycosylase activity in the context of
## methylated or unmethylated CpG sites

For its G:T mismatch-specific glycosylase activity,
10    MED1 is similar to the above mentioned Mig.Mth and the
human mismatch-specific thymine glycosylase TDG, in that
all 3 enzymes would counteract mutagenesis by spontaneous
deamination of 5-methyl-cytosine to thymine, which would
give rise to a G:T mismatch.  A model of the antimutagenic
15    activity of MED1 is shown in Figure 24.  Because cytosine
methylation in mammalian cells occurs exclusively at CpG
sites, we investigated whether a cytosine or 5-
methylcytosine preceding the mismatched guanine is a
prerequisite for MED1 thymine glycosylase activity. MED1
20    was incubated with oligonucleotide substrates in which the
mismatched G followed A, C, G, T or 5-methylcytosine (M).
As shown in Fig. 25, thymine glycosylase activity was high
with CpG/TpG and MpG/TpG substrates and low with ApG/TpT,
GpG/TpC and TpG/TpA substrates.  Interestingly, no
25    significant difference in activity was observed if
cytosine or 5-methylcytosine preceded the mismatched
guanine  (Fig. 25).  Thus, the fact that CpG/TpG and
MpG/TpG are the optimal substrates for MED1 thymine
glycosylase activity confirms that MED1 may counteract
30    mutagenic consequences of deamination of 5-methylcytosine
to thymine at CpG sites (Figure 24).


## The catalytic domain of MED1 is sufficient for glycosylase
## activity

35    The preferential activity of MED1 on substrates

presenting a G:T mismatch within the context of a CpG site raises the possibility that recognition of methylated DNA by the MBD domain is important for MED1 glycosylase activity. To test this possibility, we compared the thymine glycosylase activities of wildtype MED1 and a recombinant deletion mutant lacking the MBD and encompassing only the catalytic domain (amino acids 455-580). Both CpG/TpG and MpG/TpG substrates were processed with similar efficiency (Fig. 26 and data not shown). Thus, the catalytic domain of MED1 is sufficient for glycosylase activity, whereas the MBD is dispensable.

## MED1 is a G:U mismatch-specific uracil glycosylase active also on 5-fluorouracil

Both Mig.Mth and TDG possess mismatch-specific uracil glycosylase activity. Based on the similarities with these enzymes, we tested the uracil glycosylase activity of MED1 on oligonucleotide substrates in which uracil was paired with A, C, G and T. As expected, MED1 uracil glycosylase activity is specific for G:U mismatches (Fig. 27). MED1 did not exhibit uracil glycosylase activity on single-stranded DNA (data not shown). MED1 efficiently removed the uracil analog 5-fluorouracil (F) in the context of a G:F mismatch (Fig. 28). This finding suggests that MED1 may be involved in the resistance/tolerance to 5-fluorouracil, an agent commonly used in the treatment of colorectal cancer.

## MED1 acts as a 3, $N^4$-ethenocytosine glycosylase

It has been reported that human TDG and its *E. coli* homologue mismatch uracil glycosylase, Mug, recognize and efficiently remove 3, $N^4$-ethenocytosine (E). E is an exocyclic adduct formed by the reaction with DNA of metabolites of carcinogenic compounds, such as vinyl chloride and ethyl carbamate. Incubation of MED1 with

oligonucleotide substrates, containing E paired with G unveiled a weak E glycosylase activity (Fig. 29).

## EXAMPLE VI

5  **Detection of transition single-nucleotide polymorphisms at CpG sites (CpG transition SNPs or CT-SNPs) with MED1.**

The most efficient mechanism for repairing a damaged or mismatched base is via a glycosylase reaction which
10  removes the base, leaving an apurinic/apyrimidinic (AP) site.  The AP site may then be further processed by AP lyase (or AP endonuclease) activity in order to create a 3' OH end suitable for incorporation of an undamaged or matched nucleotide by a DNA polymerase.
15  The catalytic domain of MED1 bears distant homology to several bacterial DNA repair glycosylases/lyases.  By using recombinant MED1 protein and double-strand oligonucleotide substrates, we have shown that MED1 has a thymine and uracil glycosylase activity that specifically
20  removes thymine and uracil from G:T and G:U mismatches, respectively (see previous example). This is a function similar to that of the human thymine glycosylase TDG and its bacterial homologue Mug.

By using kinetic analyses, we have shown that MED1
25  has high glycosylase activity on G:T and G:U mismatches and weak activity on $3, N^4$-ethenocytosine, a cyclic adduct of cytosine formed by vinyl chloride and other industrial carcinogens (see previous example).  Thus, MED1 displays the following substrate preference: G:U > G:T >> G:E
30  (where E is $3, N^4$-ethenocytosine).  This substrate profile is comparable to those of TDG and Mug, which are G:U > G:E >> G:T  and  G:E  > G:U >> G:T, respectively (Saparbaev and Laval, 1998).  Thus, MED1 appears to have a marked preference for G:T substrates (Petronzelli et al.
35  submitted)

Based on its G:T mismatch-specific glycosylase activity at CpG sites (Fig. 25, previous example), MED1 would counteract mutagenesis by spontaneous deamination of 5-methylcytosine to thymine (Fig. 24), which indeed would

5      give rise to a G:T mismatch. Deamination of 5-methylcytosine to thymine is a process known to occur spontaneously at measurable rates and constitutes a major mutagenic process. Indeed, as mentioned previously, CpG sites constitute mutational hot spots in many genes,

10     including the tumor suppressor gene *p53*. Deamination of 5-methylcytosine, if not repaired, would lead to C>T and G>A transitions. These transitions at CpG sites are the most frequent mutations in human cancer, including nearly 50% of all germline *p53* mutations in Li-Fraumeni syndrome

15     families and nearly 50% of all somatic *p53* mutations in colorectal cancer.

It is clear that MED1 is likely to play a fundamental role in maintaining genomic fidelity at CpG sites in mammalian cells, which require cytosine methylation for

20     gene expression regulation, but must avoid mutagenesis by spontaneous deamination of 5-methylcytosine.

Interestingly, these changes at CpG sites are also the most frequent source of human genetic variation, as demonstrated by a recent survey by the group of Dr.

25     Chakravarti on single nucleotide polymorphisms (SNPs) at candidate genes regulating blood pressure (Halushka et al. 1999).

Since this type of SNPs are associated with genome-wide methylation at CpG sites, their origin and evolution

30     is linked not only to the general mechanisms of mutagenesis, but also primarily to deamination of 5-methylcytosine. Thus, this class of SNPs may represent a special category. Based on these considerations, we propose that C>T and G>A transitions at CpG sites should

35     be named CT-SNPs (for CpG sites transition single-

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nucleotide polymorphisms).

The availability of recombinant MED1 protein affords
a general and efficient three-step method to detect CT-
SNPs in target DNA molecules. This method is based on:
1) the formation of an heteroduplex containing a G:T
mismatch; 2) cleavage of the heteroduplex on the T-
containing strand by the combined action of MED1 followed
by incubation in hot alkali; and 3) separation of the
cleaved molecules from the uncleaved molecules by
techniques known to those of ordinary skill in the art,
such as electrophoresis.

In the first step, the T-containing strand
corresponding to a given CT-SNP is detectably labeled by
means which include without limitation, radioactive,
fluorescent or chemiluminescent labels(CT-SNP probe).
This probe may be obtained from a (possibly asymmetric)
PCR reaction or may be a synthetic oligonucleotide. The
probe is then annealed to an appropriately denatured DNA
fragment containing the CT-SNP (for instance a PCR
fragment spanning the CT-SNP).

In the second step, if the annealing of the probe to
the DNA fragment generates a heteroduplex with a G:T
mismatch, incubation with recombinant MED1 (or its
catalytic domain) followed by incubation with NaOH at high
temperature will result in the cleavage of the probe at
the G:T mismatch.

In the third step, the cleaved probe can be detected
by a variety of separation techniques, e.g.,
electrophoresis on denaturation (sequencing)
polyacrylamide gel. This three-step method is
schematically represented in Fig. 30.

This system requires a single CT-SNP probe for every
CT-SNP to analyze. Multiple CT-SNP probes could be used
to analyze a single PCR fragment containing multiple CT-
SNPs, as long as the cleaved products generated by

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incubation with MED1 are of different length or differentially labeled (e.g., with different fluorescent dyes).

A similar method, albeit with perhaps reduced specificity, could be devised with recombinant TDG or Mug.

While certain preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications may be made to the invention without departing from the scope and spirit thereof as set forth in the following claims.